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(54) **PRODUCTION OF ITACONIC ACID**

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toegepast-natuurwetenschappelijk
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2009, now Pat. No. 8,642,298.

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C12P 7/44 (2006.01)

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CPC **C12N 15/80** (2013.01); **C07K 14/38**
(2013.01); **C12P 7/44** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The invention relates to a nucleic acid sequence encoding an
itaconate transporting Major Facilitator Superfamily Trans-
porter (MFST) gene sequence and the protein encoded
thereby. Preferably said sequence is the nucleic acid that
comprises the sequence of ATEG_09972.1 of *Aspergillus*
terreus or homologues thereof. Overexpression of the protein
enhances the production of itaconic acid in micro-organisms.

11 Claims, 6 Drawing Sheets

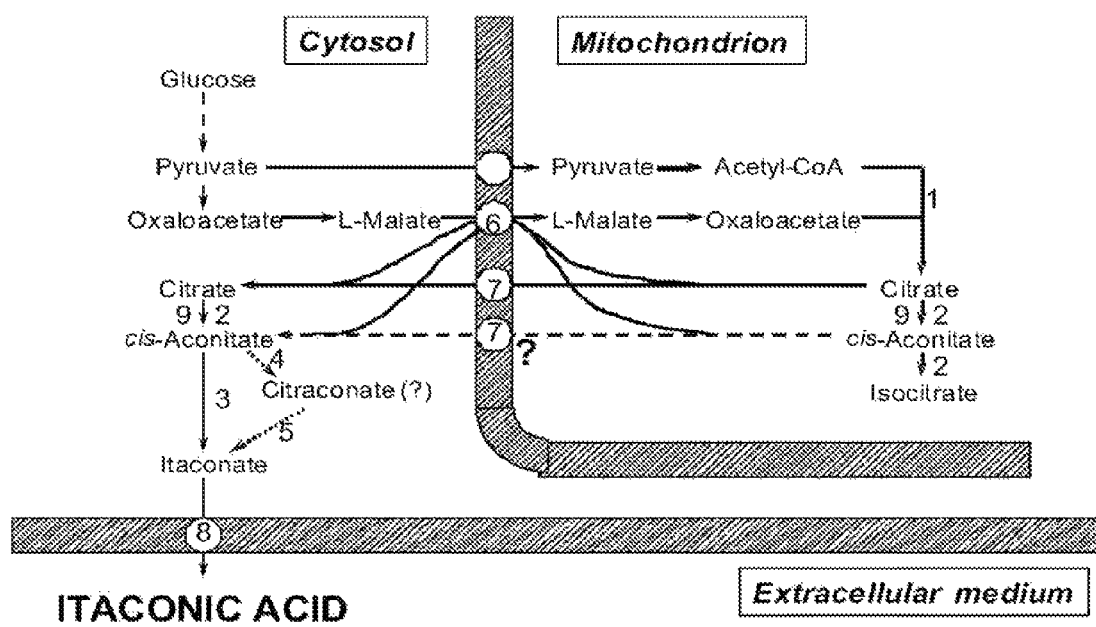


Fig. 1

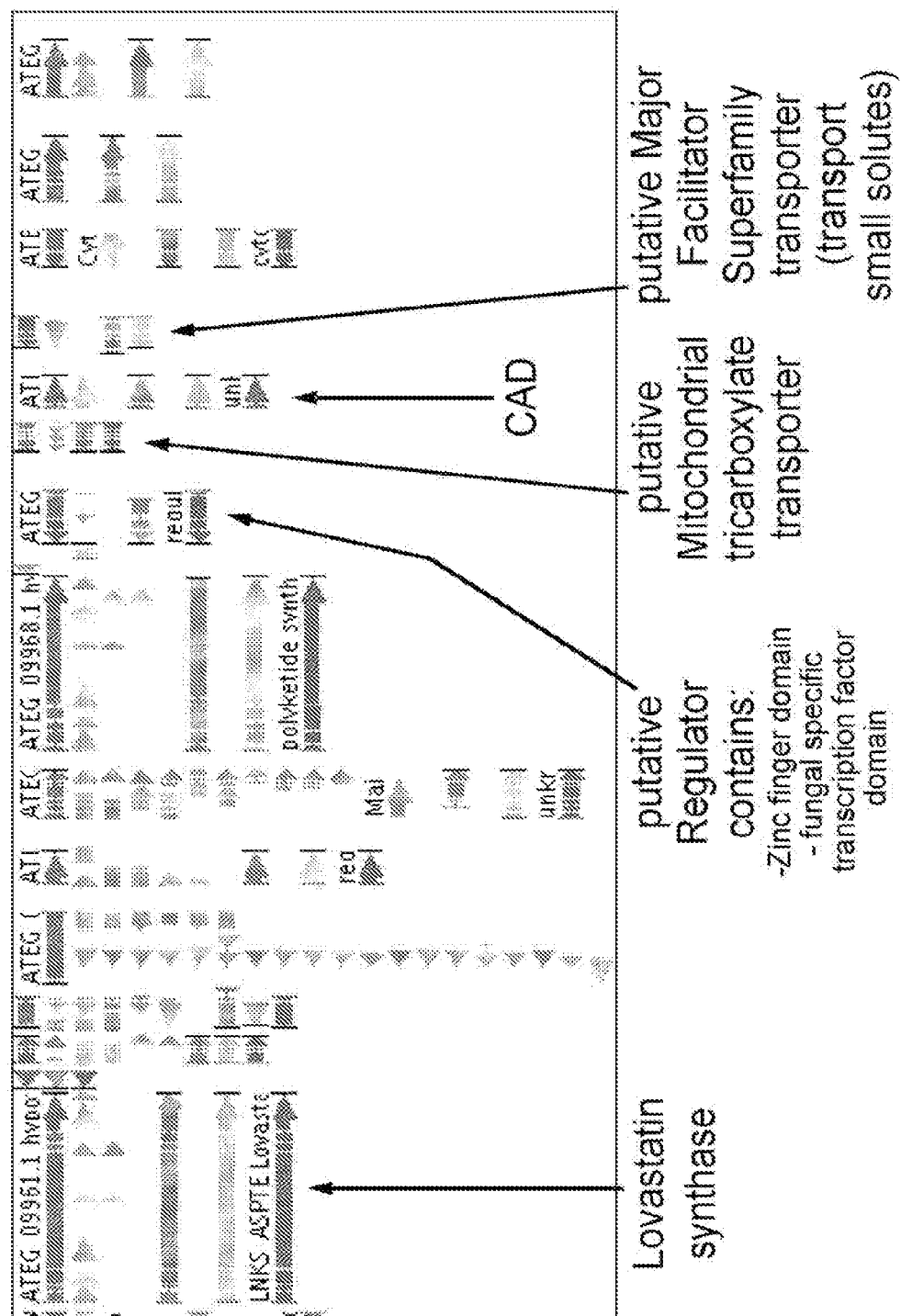


Fig. 2

Fig. 3A Amino acid sequence of ATEG_09972.1

MCHGDTESPNPTTTTEGSGQNEPEKKGRDIPLWRKCVITFVVSWMTLVVTFSSSTCLLPAA
PEIANEFDMTVETINISNAGVLVAMGYSSLIWGP MNKLVGRRTSYNLAISMLCACSAGTA
AAINEEMFLAPRVLSGLTGTSMVSGQTVLADIFEPVYRGTA VCGFFMAGT LSGPAIGPCV
GGVIVTFTSWRVIFWLQLGMSG LGLVLSLLFFPKIEGNSEKVSTAFKPTTLVTIISKFSF
TDVLKQWVYPNVFLADLCCGLLAITQYSILTSARAI FNSRFHLTTALVSGLFYLA PGAGF
LIGSLVGGKLSDRTVRRYIVKRGFRLPQDR LHSGLITLFAVLPA GTLIYGWTLQEDK GDM
VVPIIAAFFAGWGLMG SFNCLNTYVAGLFHTLIYLFPLCTCPQ*

Fig. 3B cDNA sequence of ATEG_09972.1

ATGGGCCACGGTGACACTGAGTCCCCGAACCCAACGACGACCACGGAAGGTAGCCGACAA
AACGAGCCAGAGAAAAAGGGCCGTGATATCCATTATGGAGAAAATGTGT CATTACGTTT
GTTGTTAGTTGGATGACTCTAGTCGTTACTTTCTCCAGTACTTGTCTTCTTCTCCGCGCC
CCTGAAATCGCGAATGAATTTGATATGACTGTCTGAGACTATCAACATCTCCAATGCTGGT
GTCCTAGTTGCCATGGGATATTCATCCCTCATATGGGGTCCCATGAACAAGTTAGTCGGC
CGGCGGACATCATACAATCTGGCCATTTCAATGCTTTGTGCATGCTCCGCTGGAACGGCA
GCGGCGATAAACGAGGAAATGTT CATAGCGTTCAGAGTGTTGAGCGGCTTAACCGGAACC
TCGTT CATGGTCTCAGGCCAAACTGTTCTTGCAGATATCTTTGAGCCTGTTTACCGTGGG
ACGCGCGTAGETTTCTTCATGGCCGGGACTCTTTCTGGCCCTGCAATAGGCCCCGTGCGTG
GGAGGGGT CATCGTCACTTT CACGAGTTGGCGTGTTATCTTCTGGCTTCAACTAGGTATG
AGCGGGCTGGGGCTCGTGCTTTCTCTGCTATTTTTCCCGAAAATCGAAGGAAATCTGAG
AAGGTCTCAACGGCGTTTAAACCGACCACACTTGT CACAATCATATCGAAATTTCTCCCA
ACGGATGTGCTCAAGCAGTGGGTGTATCCAAATGTCTTTCTTGCCGACTTATGCTGTGGC
CTCCTGGCAATCACGCAATATTCGATCCPGACTTCAGCTCGTGCCATATTCAACTCACGA
TTTCATTTAACGACTGCCCTAGTATCGGGTCTCTTCTACCTCGCTCCAGGTGCCGGGTTT
CTGATAGGCAGTCTCGTCCGGCGGTAAACTTTCCGATCGCACCGTTCGGAGATACATAGTA
AAGCGCGGATTCCGTCTCCCTCAGGATCGACTCCACAGCGGGCTCATCACATTGTTCCGCC
GTGCTGCCCCGAGGAACGCTCATTTACGGGTGGACACTCCAAGAGGATAAGGGTGATATG
GTAGTGCCCATAAATCGCGCGGTTCTTCGCGGGCTGGGGGCTCATGGGCAGTTTTAACTGC
CTGAACACTTACGTGGCTGGTTTGTTCCACACCCTCATTTATCTATTCCCTTTGTGTACA
TGCCCAATAA

Fig. 3C Genomic DNA sequence of ATEG_09972.1

ATGGGGCCACGGTGACACTGAGTCCCCGAACCCAACGACGACCACGGAAGGTAGCGGACAA
AACGAGCCAGAGAAAAAGGGCCCGTGATATTCATTATGGAGAAAATGTGTCAATTACGTTT
GTTGTTAGTTGGATGACTCTAGTCGTTACTTTCTCCAGTACTTGTCTTCTTCCTGCCGCC
CCTGAAATCGCGAATGAATTTGATATGACTGTCGAGACTATCAACATCTCCAATGCTGGT
GTCCTAGTTGCCATGGGATATTCATCCCTCATATGGGGTCCCATGAACAAGTTAGTCGGC
CGGCGGACATCATACAATCTGGCCATTTCAATGCTTTGTGCATGCTCCGCTGGAACGGCA
GCGGCGATAAACGAGGAAATGTTCATAGCGTTTCAGAGTGTTGAGCGGCTTAACCGGAACC
TCGTTTCATGGTCTCAGGCCAAACTGTTCTTGCAGATATCTTTGAGCCTGTACGAATCACA
CGCCCTCGTCTCCCAATTGCGAAAACATAATCCGTTCGTGCCAGGTTTACCGTGGGACG
GCCGTAGGTTTCTTCATGGCCGGGACTCTTTCTGGCCCTGCAATAGGTACGTACCCGTCT
GCAAGTACTAGAACTCCCAACAGGAACATAATTGTATGAGCAGGCCCTTCGGTGGGAGGGG
TCATCGTCACTTTACAGAGTTGGCGTGTTATCTTCTGGCTTCAACTAGGTATGAGCGGGC
TGGGGCTCGTGCTTCTCTGCTATTTTCCCGAAAATCGAAGGAAATTCAGAGAAGGTCT
CAACGGCGTTTAAACCGACCACACTTGTCACAATCATATCGAAATTCCTCCCAACGGATG
TGCTCAAGCAGTGGCTCTATCCAAATGTCTTTCTTGGCCCTAAGTGTCTGGGACATATACC
CTCTGCATCTACTGGAAAACGAGATGCTCATGCCACAAAATCAAAGGACTTATGCTGTGGC
CTCCTGGCAATCAGGCAATATTCGATCCTGACTTCAGCTCGTGCCATATTCAACTCACGA
TTTCATTTAAGCACTGCCCTAGTATCGGGTCTCTTCTACCTCGCTCCAGGTGCGGGGTTCT
CTGATAGGCAGTCTCGTGGGCGGTAAACTTTCCGATCCGACCGTTCCGAGATACATAGTA
AAGGCGGATTCCTCTCCCTCAGGATCGACTCCACAGCGGGCTCATCACATTGTTCCGC
GTGCTGCCCCAGGAACGCTCATTTACGGGTGGACACTCCAAGAGGATAAGGCTGATATG
GTAGTGGCCATAATCGCGGCGTTCTTCGCGGGCTGGGGGCTCATGGGCACTTTTAACTGC
CTGAACACTTACGTGGCTGGTTGTTCACACCCCTCATTTATCTATTCCCTTTGTGTACA
TGCCCAATAA

Fig. 4A Amino acid sequence of *A. oryzae* homologue

MGQPDLESQTPKTIIDGATKEKEEEKGSKVEKGVGLPLWRKCIILFVVSWMTLAVTFSSTSL
LPATPEIAEEFNTTETLNITNAGVLLAMGFSSLIWGPLNNLIGRRLSYNIAIFMLCVCS
AATGAAVDLKMPTAFRVLSGLTGTSFMVSGQTILADIFEPVVRGTAVGFFMAGSVSGPAI
GPCIGGLIVTFSSWRNIYWLQVGMTGFGLVLAILFVPEIKQESKESPEEKEKRTVLSALR
LFNPLRIFRQWVYPNVFFSDLTGCLLATFQYSLLSARSIFNPRFHLTTALISGLFYLPAP
GAGFLIGSIIIGKLSDRTVRKYIVRRGFRLPQDRINSGLVTLFAVLPSALIYGWTLQEE
KGGMVVPILAAFFAGWGLMGSFNTLNTYVAEALPHKRSEVIAGKYIIQYIFSAGSSALVV
PIINAIGVGWTFITCVIFSIIIGLLTMATARWGLDMQQWVERKFRIHDKPGF*

Fig. 4B cDNA sequence of *A. oryzae* homologue

atgggtcaaccocatcttgaatctcaaacccccaaaactatagacggggccacgaaagag
aaggaaagagaaaggcagcaaaagttagaaagggttacgggtcttcccttctgtggcggaatgt
atcatcctctctcgctcgctcagttggatgactcttgccggttaccttctcgagcacatctctt
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atcggtgggtctgttaacgatggctaccgcgcgatgggggtctcgatattgcaacaatgggtg
gagaggaagttccgcattcatgataaacagggttttga

Fig. 4C Genomic DNA sequence of *A. oryzae* homologue

atgggtcaaccegatcttgaatctcaaaccccccaaaactatagacgggggcccacgaaagag
aaggaagagaaaaggcagcaaagttgaaaagggttacgggtcttcctttgtggcggaatgt
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tga

PRODUCTION OF ITACONIC ACID

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a divisional of U.S. Ser. No. 12/920,461 having a U.S. filing date of Nov. 29, 2010, now U.S. Patent 8,642,298, which is the national phase of PCT application PCT/NL2009/050099 having an international filing date of Mar. 4, 2009, which claims benefit of European patent application No. 08152332.6 filed Mar. 5, 2008. The contents of the above patent applications are incorporated by reference herein in their entirety.

SUBMISSION OF SEQUENCE LISTING ON ASCII TEXT FILE

The content of the following submission on ASCII text file is incorporated herein by reference in its entirety: a computer readable form (CRF) of the Sequence Listing (file name: 313632010010SeqList.txt, date recorded: 3 Jan. 2014, size: 44,009 KB).

The invention relates to the field of microbial production, more specifically production of itaconic acid (itaconate), more specifically production of itaconate in micro-organisms.

Production and metabolism of itaconic acid in microbial cells has been studied extensively for several decades (Calam, C. T. et al., 1939, Thom. J. Biochem., 33:1488-1495; Bentley, R. and Thiessen, C. P., 1956, J. Biol. Chem. 226:673-720; Cooper, R. A. and Kornberg, H. L., 1964, Biochem. J., 91:82-91; Bonnarne, P. et al., 1995, J. Bacteriol. 117:3573-3578; Dwiarti, L. et al., 2002, J. Biosci. Bioeng. 1:29-33), but the metabolic pathway for itaconic acid has not been unequivocally established (Wilke, Th. and Vorlop, K.-D., 2001, Appl. Microbiol. Biotechnol. 56:289-295; Bonnarne, P. et al., 1995, J. Bacteriol. 177:3573-3578). Two complicating factors in this respect are that the biosynthesis route for itaconic acid is thought to occur both in the cytosol and the mitochondria (Jaklitsch, W. M. et al., 1991, J. Gen. Microbiol. Appl. 6:51-61) and that aconitase, the enzyme that interconverts citric acid into cis-aconitate, and vice versa, and other enzymes in the metabolic pathway have been found to be present in many isoforms in microbial cells.

Production of itaconic acid is now commercially achieved in *Aspergillus terreus*, which has physiological similarity to *A. niger* and *A. oryzae*. However, these latter two accumulate citric acid, due to the absence of cis-aconic acid decarboxylase (CAD) activity. Substrates used by these fungi include mono- and disaccharides, such as glucose, sucrose and fructose and starches, as they exist in forms that are degradable by the micro-organism, and molasses. Recently, it has been discovered that also glycerol is a useful substrate in itaconic acid production by *A. terreus* (U.S. Pat. No. 5,637,485).

The general scheme currently envisioned for itaconic acid biosynthesis is given in FIG. 1, wherein clearly the existence of the biosynthetic route both in the cytosol and the mitochondria is depicted and the connection between these two compartments. At several points of this scheme possibilities exist to try to improve the existing commercial production of itaconic acid in micro-organisms.

SUMMARY OF THE INVENTION

The invention comprises a nucleic acid sequence encoding an itaconate transporting Major Facilitator Superfamily Transporter (MFST) gene sequence (hereinafter "the itacon-

ate transporter"). Preferably said nucleic acid comprises the ATEG_09972.1 sequence of *Aspergillus terreus* as depicted in FIG. 3B, or a nucleic acid that shares more than about 70%, preferably more than about 80%, preferably more than about 90% sequence identity with the sequence of ATEG_09972.1 as depicted in FIG. 3b. In another embodiment, the invention comprises a protein encoded by said nucleic acid.

The invention further comprises a method for the production of itaconic acid. More specifically the invention relates to improved production of itaconic acid, comprising increasing the activity of a protein capable of transporting itaconate from the cytosol to the extracellular medium, in a suitable host cell. Preferably this is achieved by overexpression of a nucleic acid sequence encoding the protein of the invention. Preferably the said nucleic acid is derived from *Aspergillus* sp. such as, *Aspergillus terreus*, *Aspergillus niger*, *Aspergillus nidulans*, *Aspergillus oryzae* or *Aspergillus fumigatus*.

According to a further preferred embodiment, the said nucleic acid is expressed in a suitable vector, under control of its own or other promoters.

Also comprised in the invention is a method as described above, wherein the above described transport of itaconic acid is further increased by increasing the intracellular itaconic acid, using at least one but preferably a combination of the following methods:

1. overexpression of the gene coding for the enzyme CAD (see EP 07112895) which catabolises cis-aconitate to itaconic acid, preferably wherein said gene is encoded by the nucleic acid sequence of ATEG_09971.1; 2. overexpression of a gene coding for a protein capable of transporting di/tricarboxylate, preferably cis-aconitate, citrate or isocitrate, from the mitochondrion to the cytosol, more preferably the diacboxylate transporter encoded by the nucleic acid sequence of ATEG_09970.1 (see EP 08151584); 3. a method as described above, wherein the activity of a regulator protein that comprises a zinc finger and a fungal specific transcription factor domain is modulated. Preferably said regulator protein is the protein encoded by the nucleic acid sequence of ATEG_09969.1, located in the same gene cluster as the transporter of the invention. By using the above method 1 also organisms that do not or hardly produce itaconic acid like *A. niger* and *A. oryzae* due to the absence of endogenous cis-aconic acid decarboxylase (CAD) activity can be used since expression of the CAD gene will cause itaconic acid production.

Another embodiment of the present invention is formed by a host cell wherein a gene coding for an itaconate transporter is introduced. Preferably said gene comprises the nucleotide sequence of the invention encoding a transporter protein. A suitable host cell preferably is a host cell selected from filamentous fungi, yeasts and bacteria, more preferably from *Escherichia coli*, *Aspergillus* sp such as *Aspergillus niger* or *Aspergillus terreus*, citrate-producing hosts or lovastatin producing hosts. The invention further comprises a host cell as described above wherein the gene coding for a protein capable of transporting di/tricarboxylate, preferably cis-aconitate, citrate or isocitrate, from the mitochondrion to the cytosol, is co-expressed. The invention further comprises a host cell as described above, wherein the transported or produced cis-aconitate is catabolised to itaconic acid by overexpression of the gene encoding the enzyme CAD.

Further, the invention pertains to the use of the protein(s) transporting itaconate from the cytosol to the extracellular medium, for the production of itaconic acid by a suitable host cell. Also comprised in the invention is the use of said protein(s) combined with the proteins transporting di/tricarboxylate over the mitochondrial membrane, the regulator protein

ATEG_09969.2 and/or the use of the CAD enzyme, for the production of itaconic acid in a suitable host cell.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1: Postulated biosynthesis route(s) for itaconic acid in *A. terreus*. 1, Citrate synthase; 2, Aconitase; 3, cis-aconitic acid decarboxylase (itaconate-forming); 4, cis-aconitic acid decarboxylase (citraconate-forming); 5, citraconate isomerase; 6, mitochondrial dicarboxylate-tricarboxylate antiporter; 7, mitochondrial tricarboxylate transporter; 8, dicarboxylate transporter; 9, 2-methylcitrate dehydratase.

FIG. 2: Overview of *Aspergillus terreus* genome segment with the cluster of genes involved in production of itaconic acid and lovastatin ranging from ATEG_09961.1-ATEG_09975.1. The cluster contains the cis-aconitate decarboxylase (ATEG_09971.1) and the mitochondrial tricarboxylate transporter (ATEG_9970.1).

FIG. 3A-C: Sequence of the *Aspergillus terreus* itaconate transporter: FIG. 3A. protein sequence (SEQ ID NO:3), FIG. 3B. cDNA (SEQ ID NO:2), FIG. 3C. genomic sequence (SEQ ID NO:1).

FIG. 4A-C: Sequence of the *Aspergillus oryzae* itaconate transporter: FIG. 4A. protein sequence (SEQ ID NO:6), FIG. 4B. cDNA (SEQ ID NO:5), FIG. 4C. genomic sequence (SEQ ID NO:4).

DETAILED DESCRIPTION OF THE INVENTION

"Fungi" are herein defined as eukaryotic micro-organisms and include all species of the subdivision Eumycotina (Alexopoulos, C. J., 1962, In: Introductory Mycology, John Wiley & Sons, Inc., New York). The term fungus thus includes both filamentous fungi and yeast. "Filamentous fungi" are herein defined as eukaryotic micro-organisms that include all filamentous forms of the subdivision Eumycotina. These fungi are characterized by a vegetative mycelium composed of chitin, cellulose, and other complex polysaccharides. The filamentous fungi used in the present invention are morphologically, physiologically, and genetically distinct from yeasts. Vegetative growth by filamentous fungi is by hyphal elongation and carbon catabolism of most filamentous fungi are obligately aerobic. "Yeasts" are herein defined as eukaryotic micro-organisms and include all species of the subdivision Eumycotina that predominantly grow in unicellular form. Yeasts may either grow by budding of a unicellular thallus or may grow by fission of the organism.

The term "fungal", when referring to a protein or nucleic acid molecule thus means a protein or nucleic acid whose amino acid or nucleotide sequence, respectively, naturally occurs in a fungus.

The term "gene", as used herein, refers to a nucleic acid sequence containing a template for a nucleic acid polymerase, in eukaryotes, RNA polymerase II. Genes are transcribed into mRNAs that are then translated into protein.

"Expression" refers to the transcription of a gene into structural RNA (rRNA, tRNA) or messenger RNA (mRNA) with subsequent translation into a protein.

The term "vector" as used herein, includes reference to an autosomal expression vector and to an integration vector used for integration into the chromosome.

The term "expression vector" refers to a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of interest under the control of (i.e., operably linked to) additional nucleic acid segments that provide for its transcription. Such additional segments may include promoter and terminator sequences, and may optionally include

one or more origins of replication, one or more selectable markers, an enhancer, a polyadenylation signal, and the like. Expression vectors are generally derived from plasmid or viral DNA, or may contain elements of both. In particular an expression vector comprises a nucleotide sequence that comprises in the 5' to 3' direction and operably linked: (a) a yeast-recognized transcription and translation initiation region, (b) a coding sequence for a polypeptide of interest, and (c) a yeast-recognized transcription and translation termination region. "Plasmid" refers to autonomously replicating extrachromosomal DNA which is not integrated into a microorganism's genome and is usually circular in nature.

An "integration vector" refers to a DNA molecule, linear or circular, that can be incorporated in a microorganism's genome and provides for stable inheritance of a gene encoding a polypeptide of interest. The integration vector generally comprises one or more segments comprising a gene sequence encoding a polypeptide of interest under the control of (i.e., operably linked to) additional nucleic acid segments that provide for its transcription. Such additional segments may include promoter and terminator sequences, and one or more segments that drive the incorporation of the gene of interest into the genome of the target cell, usually by the process of homologous recombination. Typically, the integration vector will be one which can be transferred into the host cell, but which has a replicon that is nonfunctional in that organism. Integration of the segment comprising the gene of interest may be selected if an appropriate marker is included within that segment.

"Transformation" and "transforming", as used herein, refer to the insertion of an exogenous polynucleotide into a host cell, irrespective of the method used for the insertion, for example, direct uptake, transduction, f-mating or electroporation. The exogenous polynucleotide may be maintained as a non-integrated vector, for example, a plasmid, or alternatively, may be integrated into the host cell genome.

By "host cell" is meant a cell that contains a vector or recombinant nucleic acid molecule and supports the replication and/or expression of the vector or recombinant nucleic acid molecule. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, fungus, plant, insect, amphibian, or mammalian cells. Preferably, host cells are fungal cells.

Key in the biosynthetic pathway for itaconic acid is the localisation of the various substrates. It is thought that production of itaconic acid mainly occurs in the cytosol (see FIG. 1). In many biochemical pathways, the end-product is inhibiting its own production to prevent excess end-product in the biological system. Excess end-product will not only lead to loss of energy in an economical sense, it can also give rise to unwanted side effects such as toxicity. It is contemplated that by depleting the cell of itaconic acid the formation of new itaconic acid will continue without end-product inhibition, thus giving—in total—an increase yield of itaconic acid. Additionally the present invention enables a more simple way of harvesting the itaconic acid due to its presence in the extracellular medium. This also enables continuous fermentation culture.

Also provided are functional homologues of the ATEG_09972.1 sequences, that are 50% or more identical to the sequence of FIG. 3b, preferably 60% or more, more preferably 70% or more, more preferably 80% or more, more preferably 90% or more and most preferably 95% or more identical. Functional in the term functional homologues means that the homologous protein has an itaconic acid/itaconate transporter function i.e. is able to transport itaconate over the cell membrane.

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The term “sequence identity,” as used herein, is generally expressed as a percentage and refers to the percent of amino acid residues or nucleotides, as appropriate, that are identical as between two sequences when optimally aligned. For the purposes of this invention, sequence identity means the sequence identity determined using the well-known Basic Local Alignment Search Tool (BLAST), which is publicly available through the National Cancer Institute/National Institutes of Health (Bethesda, Md.) and has been described in printed publications (see, e.g., Altschul et al., J. Mol. Biol., 215(3), 403-10 (1990)). Preferred parameters for amino acid sequences comparison using BLASTP are gap open 11.0, gap extend 1, Blosom 62 matrix.

Every nucleic acid sequence herein that encodes a polypeptide also, by reference to the genetic code, describes every possible silent variation of the nucleic acid. The term “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or conservatively modified variants of the amino acid sequences due to the degeneracy of the genetic code.

The term “degeneracy of the genetic code” refers to the fact that a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations” and represent one species of conservatively modified variation.

The present inventors have found a method for increasing the production of itaconic acid, by increasing the activity of the protein capable of transporting itaconate from the cytosol to the extracellular medium, leading to increased recovery of itaconic acid, produced by a suitable micro-organism. The protein is further defined as a protein capable of transporting itaconic acid.

Preferably, the itaconate transporter is the itaconate transporter of *Aspergillus terreus*, as is found in the itaconate/lovastatin gene cluster (see FIG. 2), which is represented by the nucleic acid sequence found in ATEG_09972.1, which is disclosed in FIGS. 3b and 3c, for the cDNA and genomic sequence, respectively.

Further example of an itaconate transporter that could also be used in the present invention is the homologous gene denominated BAE57135.1 from *A. oryzae*, as depicted in FIGS. 4a, 4b and 4c. The produced itaconic acid can be recovered from the extracellular medium using methods known to a person skilled in the art and as described by Wilke et al. (Wilke, Th. and Vorlop, K.-D., 2001, Appl. Microbiol. Biotechnol. 56:289-295). One preferred way of increasing the activity of said protein(s) is by overexpression of a gene(s) encoding said protein(s), preferably wherein said gene is ATEG_09972.1.

Overexpression can be effected in several ways. It can be caused by transforming the micro-organism with a gene coding for the enzyme. Alternatively, other methods can be used for effecting an increase in the activity of said enzyme. One possible way is to provide a stronger promoter in front of and regulating expression of the endogenous gene. This can be achieved by use of a strong heterologous promoter or by providing mutations in the endogenous promoter. An increased activity of the enzyme can also be caused by removing possible inhibiting regulatory proteins, e.g. by inhibiting

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the expression of such proteins. The person skilled in the art will know other ways of increasing the activity of the above mentioned enzyme.

The production of itaconic acid can be further optimised by combining the product secretion and recovery as described above, with overexpression of di/tricarboxylate transporters, capable of transporting, among others, cis-aconitate, citrate or isocitrate from the mitochondrion to the cytosol, preferably the gene encoded by the nucleic acid sequence of ATEG_09970.1. These subsequent processes will lead to an increase in cis-aconitate in the cytosol, which can be further converted to itaconic acid, using overexpression of the gene encoding the enzyme CAD (EC 4.1.1.6). “CAD” is defined as the enzyme, or a nucleotide sequence encoding for the enzyme cis-aconitate decarboxylase (CAD), such as the enzyme encoded by the nucleic acid sequence of ATEG_09971.1, this further comprises enzymes with similar activities (see EP07112895).

Even further optimisation of the present invention can be achieved by modulating the activity of the regulator protein that comprises a zinc finger and a fungal specific transcription factor domain as can be found on the gene cluster that also comprises ATEG_09970, wherein this regulator protein is indicated as ATEG_09969.1 (see FIG. 2).

The above described processes alone or in combination lead to a subsequent increase of itaconic acid (see FIG. 1). Another advantage of the invention is an improved method to recover the produced itaconic acid by increasing the release in the extracellular media. The combination of improved production and improved recovery leads to an increase in itaconic acid yield by a suitable host. The above described genes are preferably derived from *Aspergillus* sp. like, *Aspergillus terreus*, *Aspergillus niger*, *Aspergillus nidulans*, *Aspergillus oryzae* or *Aspergillus fumigatus*. However, it is also possible to derive the gene from other itaconate producing micro-organisms such as *Ustilago zeae*, *Ustilago maydis*, *Ustilago* sp., *Pseudozyma antarctica*, *Candida* sp., *Yarrowia lipolytica*, and *Rhodotorula* sp.

In another aspect of the invention, micro-organisms overexpressing at least one but alternatively a combination of the above mentioned nucleotide sequences, encoding at least a protein capable of transporting itaconate from the cytosol to the extracellular medium, are produced and used for increased production of itaconic acid. More preferably micro-organisms overexpressing a protein that transports itaconate combined with protein(s) that transport di/tricarboxylates from the mitochondrion to the cytosol and/or the CAD enzyme are used to further improve the production of itaconic acid.

Micro-organisms used in the invention are preferably micro-organisms that naturally produce itaconic acid. Preferably overexpression of the genes encoding the above described protein(s) and enzyme(s) is accomplished in filamentous fungi, yeasts and/or bacteria, such as, but not limited to *Aspergillus* sp., such as the fungi *A. terreus*, *A. itaconicus* and *A. niger*, *Aspergillus nidulans*, *Aspergillus oryzae* or *Aspergillus fumigatus*, *Ustilago zeae*, *Ustilago maydis*, *Ustilago* sp., *Candida* sp., *Yarrowia lipolytica*, *Rhodotorula* sp. and *Pseudozyma antarctica*, the bacterium *E. coli* and the yeast *Saccharomyces cerevisiae*. Especially preferred are heterologous citric acid producing organisms in which the substrates are available in the host organism.

Recently (see US 2004/0033570) it has also been established that the so-called D4B segment of *Aspergillus terreus*, which comprises the CAD gene is responsible for the synthesis of lovastatin (see FIG. 2). Thus, it is submitted that also these micro-organisms which are known to produce lovasta-

tin would be suitable candidates for the production of itaconic acid. Such micro-organisms include *Monascus* spp. (such as *M. ruber*, *M. purpureus*, *M. pilosus*, *M. vitreus* and *M. pubigerus*), *Penicillium* spp. (such as *P. citrinum*, *P. chrysogenum*), *Hypomyces* spp., *Doratomyces* spp. (such as *D. stemonitis*), *Phoma* spp., *Eupenicillium* spp., *Gymnoascus* spp., *Pichia labacensis*, *Candida cariosilignicola*, *Paecilomyces virioli*, *Scopulariopsis brevicaulis* and *Trichoderma* spp. (such as *T. viride*).

Consequently also the CAD encoding part of the D4B segment and the enzyme with CAD activity for which it codes from these above-mentioned lovastatin producing micro-organisms are deemed to be suitable for use in the present invention. It further is contemplated that a heterologous organism, which in nature does not or hardly produce itaconic acid like *Aspergillus niger* or *Aspergillus oryzae* can be used when providing such an organism with a functional pathway for expression of itaconic acid, by overexpression of the above mentioned genes.

Recombinant host cells described above can be obtained using methods known in the art for providing cells with recombinant nucleic acids. These include transformation, transconjugation, transfection or electroporation of a host cell with a suitable plasmid (also referred to as vector) comprising the nucleic acid construct of interest operationally coupled to a promoter sequence to drive expression. Host cells of the invention are preferably transformed with a nucleic acid construct as further defined below and may comprise a single but preferably comprises multiple copies of the nucleic acid construct. The nucleic acid construct may be maintained episomally and thus comprise a sequence for autonomous replication, such as an ARS sequence. Suitable episomal nucleic acid constructs may e.g. be based on the yeast 2 μ or pKD1 (Fleer et al., 1991, Biotechnology 9: 968-975) plasmids. Preferably, however, the nucleic acid construct is integrated in one or more copies into the genome of the host cell. Integration into the host cell's genome may occur at random by illegitimate recombination but preferably the nucleic acid construct is integrated into the host cell's genome by homologous recombination as is well known in the art of fungal molecular genetics (see e.g. WO 90/14423, EP-A-0 481 008, EP-A-0 635 574 and U.S. Pat. No. 6,265,186) Most preferably for homologous recombination the ku70 Δ /ku80 Δ , techniques is used as described for instance in WO 02/052026 and Krappmann, 2007, Fungal Biol. Rev. 21:25-29).

Transformation of host cells with the nucleic acid constructs of the invention and additional genetic modification of the fungal host cells of the invention as described above may be carried out by methods well known in the art. Such methods are e.g. known from standard handbooks, such as Sambrook and Russel (2001) "Molecular Cloning: A Laboratory Manual (3rd edition), Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, or F. Ausubel et al, eds., "Current protocols in molecular biology", Green Publishing and Wiley Interscience, New York (1987). Methods for transformation and genetic modification of fungal host cells are known from e.g. EP-A-0 635 574, WO 98/46772, WO 99/60102 and WO 00/37671.

In another aspect the invention relates to a nucleic acid construct comprising a nucleotide sequence encoding at least an itaconate transporter as defined above and usable for transformation of a host cell as defined above. In the nucleic acid construct, the coding nucleotide sequence(s) preferably is/are operably linked to a promoter for control and initiation of transcription of the nucleotide sequence in a host cell as defined below. The promoter preferably is capable of causing sufficient expression of the itaconate transporters transport-

ing itaconate from the cytosol to the extracellular medium and/or the di/tricarboxylate transporters transporting tricarboxylates from the mitochondrion and/or the CAD enzyme(s), described above, in the host cell. Promoters useful in the nucleic acid constructs of the invention include the promoter that in nature provides for expression of the coding genes. Further, both constitutive and inducible natural promoters as well as engineered promoters can be used. Promoters suitable to drive expression of the genes in the hosts of the invention include e.g. promoters from glycolytic genes (e.g. from a glyceraldehyde-3-phosphate dehydrogenase gene), ribosomal protein encoding gene promoters, alcohol dehydrogenase promoters (ADH1, ADH4, and the like), promoters from genes encoding amylolytic or cellulolytic enzymes (glucoamylase, TAKA-amylase and cellobiohydrolase). Other promoters, both constitutive and inducible and enhancers or upstream activating sequences will be known to those of skill in the art. The promoters used in the nucleic acid constructs of the present invention may be modified, if desired, to affect their control characteristics. Preferably, the promoter used in the nucleic acid construct for expression of the genes is homologous to the host cell in which genes are expressed.

In the nucleic acid construct, the 3'-end of the coding nucleotide acid sequence(s) preferably is/are operably linked to a transcription terminator sequence. Preferably the terminator sequence is operable in a host cell of choice. In any case the choice of the terminator is not critical; it may e.g. be from any fungal gene, although terminators may sometimes work if from a non-fungal, eukaryotic, gene. The transcription termination sequence further preferably comprises a polyadenylation signal.

Optionally, a selectable marker may be present in the nucleic acid construct. As used herein, the term "marker" refers to a gene encoding a trait or a phenotype which permits the selection of, or the screening for, a host cell containing the marker. A variety of selectable marker genes are available for use in the transformation of fungi. Suitable markers include auxotrophic marker genes involved in amino acid or nucleotide metabolism, such as e.g. genes encoding ornithine-transcarbamylases (*argB*), orotidine-5'-decarboxylases (*pyrG*, *URA3*) or glutamine-amido-transferase indoleglycerol-phosphate-synthase phosphoribosyl-anthranilate isomerases (*trpC*), or involved in carbon or nitrogen metabolism, such e.g. *niaD* or *facA*, and antibiotic resistance markers such as genes providing resistance against phleomycin, bleomycin or neomycin (G418). Preferably, bidirectional selection markers are used for which both a positive and a negative genetic selection is possible. Examples of such bidirectional markers are the *pyrG* (*URA3*), *facA* and *amdS* genes. Due to their bidirectionality these markers can be deleted from transformed filamentous fungus while leaving the introduced recombinant DNA molecule in place, in order to obtain fungi that do not contain selectable markers. This essence of this MARKER GENE FREE™ transformation technology is disclosed in EP-A-0 635 574, which is herein incorporated by reference. Of these selectable markers the use of dominant and bidirectional selectable markers such as acetamidase genes like the *amdS* genes of *A. nidulans*, *A. niger* and *P. chrysogenum* is most preferred. In addition to their bidirectionality these markers provide the advantage that they are dominant selectable markers that, the use of which does not require mutant (auxotrophic) strains, but which can be used directly in wild type strains.

Optional further elements that may be present in the nucleic acid constructs of the invention include, but are not limited to, one or more leader sequences, enhancers, integration factors, and/or reporter genes, intron sequences, cen-

tromers, telomers and/or matrix attachment (MAR) sequences. The nucleic acid constructs of the invention may further comprise a sequence for autonomous replication, such as an ARS sequence. Suitable episomal nucleic acid constructs may e.g. be based on the yeast 2 μ or pKD1 (Fleer et al., 1991, Biotechnology 9: 968-975) plasmids. Alternatively the nucleic acid construct may comprise sequences for integration, preferably by homologous recombination (see e.g. WO98/46772). Such sequences may thus be sequences homologous to the target site for integration in the host cell's genome. The nucleic acid constructs of the invention can be provided in a manner known per se, which generally involves techniques such as restricting and linking nucleic acids/nucleic acid sequences, for which reference is made to the standard handbooks, such as Sambrook and Russel (2001) "Molecular Cloning: A Laboratory Manual (3rd edition), Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, or F. Ausubel et al, eds., "Current protocols in molecular biology", Green Publishing and Wiley Interscience, New York (1987).

In a further aspect the invention relates to fermentation processes in which the transformed host cells of the invention are used for the conversion of a substrate into itaconic acid. A preferred fermentation process is an aerobic fermentation process. The fermentation process may either be a submerged or a solid state fermentation process.

In a solid state fermentation process (sometimes referred to as semi-solid state fermentation) the transformed host cells are fermenting on a solid medium that provides anchorage points for the fungus in the absence of any freely flowing substance. The amount of water in the solid medium can be any amount of water. For example, the solid medium could be almost dry, or it could be slushy. A person skilled in the art knows that the terms "solid state fermentation" and "semi-solid state fermentation" are interchangeable. A wide variety of solid state fermentation devices have previously been described (for review see, Larroche et al., "Special Transformation Processes Using Fungal Spores and Immobilized Cells", Adv. Biochem. Eng. Biotech., (1997), Vol 55, pp. 179; Roussos et al., "Zymotis: A large Scale Solid State Fermenter", Applied Biochemistry and Biotechnology, (1993), Vol. 42, pp. 37-52; Smits et al., "Solid-State Fermentation-A Mini Review, 1998), Agro-Food-Industry Hi-Tech, March/April, pp. 29-36). These devices fall within two categories, those categories being static systems and agitated systems. In static systems, the solid media is stationary throughout the fermentation process. Examples of static systems used for solid state fermentation include flasks, petri dishes, trays, fixed bed columns, and ovens. Agitated systems provide a means for mixing the solid media during the fermentation process. One example of an agitated system is a rotating drum (Larroche et al., supra). In a submerged fermentation process on the other hand, the transformed fungal host cells are fermenting while being submerged in a liquid medium, usually in a stirred tank fermenter as are well known in the art, although also other types of fermenters such as e.g. airlift-type fermenters may also be applied (see e.g. U.S. Pat. No. 6,746,862).

Preferred in the invention is a submerged fermentation process, which is performed in a fed-batch or repeated (fed)-batch mode. In a fed-batch fermentation there is a continuous input of feed containing a carbon source and/or other relevant nutrients in order to improve itaconic acid yields. The input of the feed can, for example, be at a constant rate or when the concentration of a specific substrate or fermentation parameter falls below some set point. In a repeated batch fermentation the culture is harvested at regular time-intervals by

stopping the fermentation and retrieving the produced product from the medium. Next to refreshing the medium often also part of the microbial culture is discarded, while the rest is used as a new inoculum for a following batch culture.

It is preferred to use a host cell that naturally would contain the enzymes/transporters of the itaconic acid pathway as depicted in FIG. 1, and the enzymes/transporters of the citric acid pathways in the cytosol and mitochondrion. However, if the host would lack one or more of these genes, they can be co-introduced with the above described enzymes and proteins. Such a co-introduction can be performed by placing the nucleotide sequence of such a gene on the same plasmid vector as the above described genes, or on a separate plasmid vector.

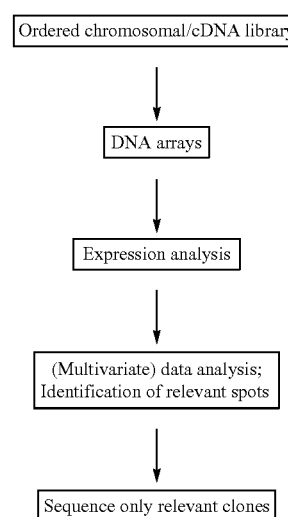
Further, since the itaconic acid pathway is located partly in the cytosol and partly in the mitochondrion, it is contemplated that overexpression of the genes/enzymes in either or both of those compartments would be desirable. The person skilled in the art will know how to achieve overexpression in the cytosol or mitochondria by using the appropriate signal sequences.

EXAMPLES

Example 1

Construction of Micro-Array

An anonymous clone/EST-based array approach was taken according to the following scheme:



An *A. terreus* micro-array was made composed of a clone-based and an EST-based array.

Materials and Methods Construction Micro-Array

Isolation of Chromosomal DNA from *A. Terreus*

A. terreus was cultivated overnight in a shake flask in enriched minimal medium at 33° C. and 250 rpm. Enriched minimal medium (pH 5.5) is mineral medium (MM) supplemented with 0.5% yeast extract and 0.2% casamino acids. The composition of MM was: 0.07 M NaNO₃, 7 mM KCl, 0.11 M KH₂PO₄, 2 mM MgSO₄, and 1 ml/1 of trace elements (1000* stock solution: 67 mM ZnSO₄, 178 mM H₃BO₃, 25 mM MnCl₂, 18 mM FeSO₄, 7.1 mM CoCl₂, 6.4 mM CuSO₄, 6.2 mM Na₂MoO₄, 174 mM EDTA).

Mycelium was harvested after 22 hours and frozen in liquid nitrogen. Chromosomal DNA was isolated from 4.5 g mycelium following the protocol described below.

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Grind 0.5-1.0 g mycelium under liquid nitrogen using the membrane disrupter.

Place polypropylene tubes (Greiner) with 1.5 ml water-saturated phenol, 1 ml TNS, 1 ml PAS and 0.5 ml 5xRNB in a water bath at 55° C., add the still frozen mycelium to the tubes and vortex every 20 seconds for totally 2-4 minutes.

TNS: triisopropyl naphthalene sulphonic acid, 20 mg/ml in water, freshly prepared

PAS: 4 aminosalicylic acid, 120 mg/ml in water, freshly prepared

5xRNB: 60.55 g Tris, 36.52 g NaCl, 47.55 g EGTA in 500 ml water (pH=8.5)

Add 1 ml sevag (24:1 chloroform:isoamyl alcohol) and vortex with intervals for another 1-2 minutes.

Spin for 10 min. in the tabletop centrifuge at 4° C. at maximum velocity.

Extract the water-phase once again with phenol-sevag and twice with sevag. GENTLY, AVOID SHEARING!

Precipitate the DNA with 2 volumes ethanol. Spin directly for 10 min. in the tabletop centrifuge.

Drain the tube, dry it with Kleenex and resuspend the pellet in 500 µl Tris/EDTA. Transfer to a microvial.

Extract with phenol-sevag until interface stays clean. Then extract once with sevag.

Precipitate with 2 volumes ice-cold ethanol, spin down and resuspend the pellet in 100-200 µl TE with 50 µg/ml RNase.

Construction of Clone-Based gDNA Library

The gDNA library was prepared as follows:

Chromosomal *A. terreus* DNA was sheared into fragments of size 1.5-2.5 kb

The sheared DNA was subsequently size fractionated, end-repaired (Lucigen), and ligated into blunt-end pSMART-HC-Amp vectors (Lucigen).

The ligated constructs were transformed into *E. coli* DH 10b

Colony PCR was performed on 96 transformants to check that >90% of the inserts had the correct size

Sequence analysis (short run) was performed on 20 clones to confirm their diversity and fungal origin

Colony picking of 20,000 amp-resistant colonies was carried out into 96-well microtiter plates containing TY medium+100 µg/ml ampicillin

The 20,000 clones were replicated into 96-well microtiter plates. The ordered libraries are stored as glycerol stocks at -80° C.

Generation of mRNA for cDNA Library Construction

Precultures: *A. terreus* spores (10^6 - 10^7 /ml) were inoculated into 100 ml B medium (2 g/l NH₄NO₃; 1 g/l MgSO₄*7H₂O; 0.008 g/l ZnSO₄*7H₂O; 0.015 g/l CuSO₄*5H₂O; 1.5 ppm FeSO₄*5H₂O; 0.08 g/l KH₂PO₄; 10 g/l CaCl₂*2H₂O, set to pH 3.1 with HCl) containing 20 g/l glucose, and incubated for 24-48 hours at 37° C. at 250 rpm. Production cultures (B medium containing 100 g/l glucose) were inoculated 1/10 (v/v) for 2-days cultivations and 1/25 (v/v) for 3-day cultivations. After 2-3 days cultivation mycelium was harvested, filtered over miracloth, washed with 0.2 M sodium phosphate buffer (pH 6.5), frozen in liquid nitrogen and stored at -80° C.

Isolation of mRNA from *A. terreus*

grind mycelium with mortar and pestle under liquid nitrogen; add 100 µl β-mercaptoethanol before grinding to inactivate RNase

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transfer powder to cooled plastic tube (1.0 g per tube); keep mycelium frozen

add 4 ml TRIzol® and vortex till homogenous

add 0.4 ml chloroform and vortex

centrifuge for 20-30 min. at 3700 rpm, 4° C.

transfer supernatant to Eppendorf™ tubes (1.2 ml per tube)

add 0.7 ml per 1.2 ml supernatant

centrifuge in Eppendorf™ centrifuge for 15 min. at 14,000 rpm, 4° C.

wash pellet with 1 ml 70% ethanol

centrifuge 5 min., 14,000 rpm, 4° C.

air-dry pellet and resuspend in 0.2 ml water

store RNA samples at -80° C.

Construction of cDNA Library

The cDNA library was prepared as follows:

The RNA was run on gel to determine the quality of the sample

polyT-primed cDNA was prepared from the total RNA provided (RT-PCR reaction using superscript and dT primers

The cDNA was size fractionated to give fragments of size 1.0-1.5 kb

The fragments were end-repaired (Lucigen), and ligated into blunt-end pSMART-HC-kan vectors (Lucigen).

Restriction analysis of 96 clones was performed to check the insert size and the % of transformants which had the correct insert size

Sequence analysis (short run) of 20 clones was performed to confirm diversity and fungal origin

5,000 kanamycin-resistant colonies were picked into microtiter plates

The 5000 cDNA clones were replicated into 96-well microtiter plates. The ordered libraries were stored as glycerol stocks at -80° C.

Construction of the *A. Terreus* Clone-Based Array

PCR fragments were generated from the different clones from the gDNA (20,000 clones) and cDNA (5,000 clones) library by mass 96 well PCR (50 µl/well, Lucigen SMART-SR1/SL1 primers with 5'-C6-aminolinkers, SuperTaq and buffer from HT Biotech. Ltd, dNTP's (Roche 11 969 064 001), pintool dipped template from grown colony plates).

All above PCR products were purified by 96 well precipitation (isopropanol and 96% ethanol wash), speedvac dried, dissolved in 15 µl 3xSSC/well and spotted with quill pins (Telechem SMP3) on CSS100 silylated aldehyde glass slides (Telechem, USA) using a SDDC2 Eurogridder (ESI, Canada). During spotting, aminolinkers of PCR products will covalently link with aldehyde groups of the coated slides.

gDNA and cDNA PCR products were spotted on two separate slides (slide a: 1st 10,000 gDNA's+5000 cDNA's; slide b: 2nd 10,000 gDNA's+same 5000 cDNA's).

For the clone-based array a genomic library was constructed. A total of 20,000 clones containing chromosomal fragments was generated, 90% of which had an average insert size of 1.5-2.5 kb. This resulted in a full genome coverage of 64% (Akopyants et al., 2001).

For the EST-based array a cDNA library of in total 5000 cDNA clones was constructed, 70% of which had an average insert size of 1.0-1.5 kb. This so-called EST-based approach has the advantage that it will be enriched for the genes expressed under the selected (itaconic acid producing) conditions. Moreover, in the EST-based approach per clone (and thus spot) only a single gene is represented in eukaryotes.

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The complete micro-array, thus consisting of 20,000 genomic DNA clones and 5,000 cDNA clones was composed of an A and a B glass slide. Both slides contained the same 5,000 cDNA spots. The A and B slide each contained 10,000 of the gDNA spots.

Example 2

Generation of the Different RNA Samples by Fermentation

Materials and Methods Fermentation and mRNA Isolation

Fermentation conditions of *A. terreus*

5-Liter controlled batch fermentations were performed in a New Brunswick Scientific Bioflow 3000 fermentors. The following conditions were used unless stated otherwise:

37° C.

pH start 3.5 set point 2.3

DO set points Day 1: 75%

Day 2, 3, 4: 50%

Subsequent days: 25%

Preculture: 100 ml of the same medium as used in the fermentation medium (10^7 spores/ml) in 500 ml Erlenmeyer flask with baffles, overnight, 37° C., 150 rpm

pH control: 4M KOH (Base), 1.5 M H_3PO_4 (Acid)

Antifoam: Struktol (Schill & Seilacher)

Fermentation Medium Compositions:

Per litre: 2.36 g of NH_4SO_4 , 0.11 g of KH_2PO_4 , 2.08 g of $MgSO_4 \cdot 7H_2O$, 0.13 g of $CaCl_2 \cdot 2H_2O$, 0.074 g of NaCl, 0.2 mg of $CuSO_4 \cdot 5H_2O$, 5.5 mg of $Fe(III)SO_4 \cdot 7H_2O$, 0.7 mg of $MnCl_2 \cdot 4H_2O$ and 1.3 mg of $ZnSO_4 \cdot 7H_2O$ and 100 g of glucose as a carbon source.

All media were prepared in demineralised water.

Isolation of mRNA from *A. terreus*

See mRNA isolation protocol described in Example 1

Determination of the Itaconate Concentration by HPLC

5 μ l of a 10-times diluted supernatant sample (split ratio 1:3) was separated using a Waters 2695 Separations module on a reversed-phase Develosil 3 μ m RP-Aqueous C30 140A column (150x3 mm) (Phenomenex p/n CH0-6001) at 25° C. using the solvent gradient profile (flow rate was 0.4 ml/min) shown in Table 1.

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TABLE 1

Solvent gradient of the RP-UV method.			
Time (min)	A (20 mM NaH_2PO_4 pH 2.25) (%)		B (Acetonitril) (%)
0	100		0
10	100		0
15	95		5
20	95		5
21	100		0
30	100		0

Compounds were detected by UV at 210 nm using a Waters 2487 Dual wavelength Absorbance detector (Milford, Mass., USA).

Itaconate Productivity

Itaconate productivity at a certain time point was calculated as the slope of the regression line between that particular time point and the time points right before and after that time point. To this end of 6-10 supernatant samples of the different fermentations, the itaconate concentrations were determined by HPLC.

For the transcriptomics approach it is essential to have RNA samples from fermentations that result in the production of different amounts of itaconate. Therefore a literature survey was performed in order to identify medium components and/or physicochemical conditions that affect the amount of itaconate produced by *A. terreus*. Although many conflicting reports were found regarding the effect that a specific parameter has on itaconic acid production, 4 key overall parameters were identified from this literature survey, i.e. (i) carbon source, (ii) pH, (iii) trace element (i.e. Mn) concentration and (iv) oxygen tension. Fermentations with *A. terreus* varying principally in these four parameters were performed on a mineral salts medium to ensure that the elemental limitations required for itaconate production would be achieved. Table 2 presents an overview of the fermentations performed in this study.

TABLE 2

Overview of the fermentations performed in order to generate RNA samples for transcriptome analysis. The reference fermentation is on 100 g/l glucose, dO ₂ , day 1, 75%; day 2-4, 50%, day 5 and further 25%, pH start 3.5, set point at 2.3.				
Fermentation run	Fermentation Environmental condition		Max. Itaconic acid (g/l)	Max. Biomass (gDWT/kg)
First Run	1	Glucose (100 g/l) (control)	16.1	12.7
	2	Fructose as C-source	8.84	13.7
	3	Maltose as C-source	13.9	12.1
Second run	4	Glucose (100 g/l) pH start 3.5, set point 2.3 (control)	25.8	11.6
	5	pH set 3.5	8.7	16.5
	6	pH start 3.5 no set point	30.6	8.7
Third run	7	Low glucose (30 g/l)	11.1	6.7
	8	O ₂ set point 25%	47.2	12.0
	9	5* higher Mn	20.3	13.8
Fourth run	10	Glucose (100 g/l) (control)	26.9	17.9
	11	pH set 4.5	0.1	20.4
	12	O ₂ set point 10%	52.9	10.6

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As shown in Table 2, a considerable variation in the amount of itaconate is produced in this set of fermentations, ranging from almost no itaconate (fermentation #11; pH 4.5) to about 50 g/l itaconate (#8 and #12; O₂ set point 25% and 10% respectively).

Of each fermentation 2 to 5 samples were harvested for isolation of mRNA.

From in total 23 fermentation samples mRNA could be isolated. Of 7 samples, mRNA was isolated twice independently. It proved to be especially difficult (impossible) to extract RNA from the samples taken in the stationary phase. A number of samples showed partial degradation of the RNA. Although no mRNA could be isolated from the samples from fermentations #6 and #12, the remaining samples still covered the complete range of itaconate production (Table 3).

TABLE 3

List of 30 mRNA samples from various fermentation conditions that were used for transcriptome analysis. The samples marked with asterisk were the samples used for the differential expression data analysis.

Sam- ple No.	Fer- mentation condition	RNA id	EFT (hours)	Itaconic acid (g/l)	Itaconic acid Productivity	RNA quality
R3	gluc100	1.3.a	50.3	14.6	0.117	ok
R4	gluc100	1.4.a	74.8	16.1	0.060	ok
R5	fruc100	2.3.a	50.3	8.2	0.082	ok
R6	fruc100	2.3.b	50.3	8.2	0.082	ok
R7	fruc100	2.4.a	75.05	8.6	-0.013	ok
R8	malt100	3.3.a	50.3	7	0.355	ok
R9	malt100	3.4.a	75	12.1	0.220	ok
R10	pH-i3.5	4.3.a	53.25	25.8	0.146	part degr
R11	pH-i3.5	4.3.b	53.25	25.8	0.146	part degr
R12	pH-i3.5	4.4.a	73	24	-0.153*	ok
R13	pH-c3.5	5.3.a	53.5	7.5	-0.042	ok
R14	pH-c3.5	5.3.b	53.5	7.5	-0.042	ok
R15	pH-c3.5	5.4.a	73.25	7.9	0.035	ok
R16	gluc30	7.2.a	30.25	9	0.317	ok
R1	gluc30	7.3.a	43.5	10	0.030	ok
R17	gluc30	7.3.a	43.5	10	0.030	ok
R18	O2s25%	8.2.a	30.5	36*	0.824*	ok
R19	O2s25%	8.4.a	78.25	46	0.029	part degr
R20	5xMn	9.2.a	30.75	1	0.194	ok
R21	5xMn	9.2.b	30.75	1	0.194	ok
R22	5xMn	9.3.a	53.5	10	0.496	part degr
R23	5xMn	9.3.b	53.5	10	0.496	part degr
R24	5xMn	9.4.a	78.5	19	0.189	part degr
R25	5xMn	9.4.b	78.5	19	0.189	part degr
R26	5xMn	9.5.a	93.25	20	0.106	ok
R2	Gluc100	10.3.a	51.5	14.7	0.256	ok
R27	Gluc100	10.3.a	51.5	14.7	0.256	ok
R28	Gluc100	10.4.a	74	19.5	0.085	ok
R29	Gluc100	10.5.a	100.4	22	0.177	part degr
R30	Gluc100	10.5.b	100.4	22	0.177	part degr
R31	pH4.5	11.3.a	51.5	0.04*	-0.001	ok
R32	pH4.5	11.4.a	74	0.05*	0.003	ok

Example 3

Transcriptome Analysis, Data Analysis of the Array Data

Materials and Methods Transcriptome Analysis, Data Normalization and Data Analysis

Labeling of RNA and gDNA

Total RNA's (5 µg/30 µl reaction), isolated from various *A. terreus* cultures (strain NRRL 1960, BASF) with differential itaconate production, were labelled with amino-allyl-dUTP

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(0.75 µM aa-dUTP final conc., Sigma A0410), using 3 µl 50 µM oligo p(dT)₁₅ primer (La Roche, 814270), unlabelled dNTP's (added to 1.25 µM final conc. for each dNTP), 2 µl Superscript II Reverse Transcriptase and buffer (Life Technologies, 10297-018: primer annealing 10 min 70° C., transcriptase 180 min 42°). After RNA hydrolysis (3 µl 2.5M NaOH, 30 min 37°, 3 µl 2.5 M HAc) the aa-dUTP labelled cDNA was directly purified (below).

As a reference for correcting slide differences (spotting, labeling-, hybridization- and scan efficiency), gDNA (0.5 µg/reaction) of *Aspergillus terreus* (strain NRRL 1960, BASF) was labelled with aa-dUTP, using dNTP's (conc. as above), Klenov-DNA Polymerase and buffer (Bioprime kit, Invitrogen 18094-011: primer annealing 5 min 96° C., polymerase 90 min 37°).

The aa-dUTP-labelled cDNA or gDNA was purified (QIAquick column, Qiagen 28106), speedvac dried, dissolved (4.5 µl 0.1 M Na₂CO₃), coupled with 4.5 µl Cy5—NHS-ester for cDNA, or 4.5 µl Cy3-NHS-ester for gDNA (Amersham/GE-Healthcare PA25001 or PA23001 respectively, each in 73 µl DMSO) for 60 min at 20° C., diluted with 10 µl of water, and again purified on Autoseq G50 columns (GE-Healthcare 27-5340).

Array Blocking, (Pre)Hybridization and Image Analysis

Before hybridization with the array produced as described above, slides were blocked (removal surplus of spotted PCR products and blocking of free aldehyde groups) by 3× quickly washing (20° C.) with PreHyb buffer and 45 min incubation (42° C.) in PreHyb buffer (5×SSC, 1% BSA, 0.1% SDS). After 4 washes in water, spotted PCR products were denatured by dipping the slides 5 sec in boiling water and drying

them with a N₂-gas-pistol.

The Cy5- and Cy3-labelled sample were combined, 8 µl 25 µg/µl yeast tRNA (Invitrogen, 15401-029) and 4 µl 5 µg/µl poly-dA/dT (Amersham 27-7860) were added, the mixture was speed vac dried, dissolved in 160 µl Easyhyb buffer (Roche, 1 796 895), denatured (2 min, 96° C.), cooled to 50° C., applied on a pair of prehybridised slides (a+b, 80 µl/slide) prewarmed at 50° C., covered with a cover slide (Hybri slibs, Mol. Probes. H-18201) and incubated overnight at 42° C. in a humidified hybridization chamber (Corning 2551). Slides were washed (pair a+b in one 50 ml tube, 1× in 1×SSC/0.1% SDS 37° C., 1× in 0.5×SSC 37° C., 2× in 0.2×SSC 20° C.) and dried with N₂-gas. All pre-hybridisation buffers were 0.45 µm filtered to reduce dust noise. Slide images of Cy5- and Cy3-fluorescence intensity (ScanArray Express Scanner & Software, Packard Biosc.) were analysed (Image 5.6 Software, Biodiscovery) to obtain for each spot signal- and local background value (medians) for the hybridized Cy5-RNA and Cy3-reference gDNA. These values were used for further data analysis.

Array Data Normalization

Before normalization, all low abundant spots having a Signal/Background below 1.5 were removed. Data were normalized using a total cDNA signal correction. For each slide and each spot, the difference between signal and background was calculated for Cy5 and Cy3. Per slide, the sum of the differences was taken for Cy5 and Cy3, and the ratio between these two was used as normalization factor for that particular slide. All spots (chromosomal and genomic) were normalised using this total cDNA signal.

Data Analysis of the Transcriptomics Data by Multivariate Regression Analysis
Scaling

Data were range scaled $(x - \bar{x}) / (x_{max} - x_{min})$ (van den Berg et al., 2006, BMC Genomics 7:142) in the statistical analysis. Mathematically, range-scaling means that every element of column i is divided by the range of column i . The range of column i is the difference between the maximum and minimum value of all elements of column i . Subsequently, the scaled dataset is mean-centered. Mathematically, mean-centering means that adding up the values of the individual elements of column i of a data matrix results in zero for column i . This is achieved by subtracting the mean of column i from all values of the individual elements of column i .

PLS Analysis

PLS analysis (Geladi and Kowalski, 1986) was performed in the Matlab environment using the PLS Toolbox (version 3.5.4, 2006; Eigenvector Research, Manson, Wash.).

It is possible that transcripts that show a lot of variation disturb the performance of the PLS model. Therefore, the model was optimized using a jack-knife approach. A model was build leaving out 10% of the samples, which was repeated until all samples were left out once. For each transcript, the relative standard deviation (RSD) was calculated and transcripts which had an RSD > 50% were left out to build a second PLS model.

Validation of the Results

A double cross-validation procedure was used to validate the PLS model. In short, two loops are defined: an inner loop and an outer loop. In the innerloop 90% of the data is used to find an optimal PLS model. In the outerloop a prediction is made for the remaining 10% of the data based on the inner-loop PLS model. This is repeated until all samples are left out once (so in this case 10 times). Goal of the DCV is to get an independent estimate of the prediction error. The R^2 was calculated to determine how good the original productivity or titer was predicted by the model. The closer the R^2 gets to 1, the better the model.

Sequence Analysis of Spots Selected after Transcriptomics Approach

The relevant clones were selected from the glycerol stocks of the ordered libraries (gDNA and cDNA library respectively) and cultivated in 96-well microtiter plates. The sequences of the inserts from both the 3' and the 5' end were determined by High Throughput (HT) sequencing service.

All RNA samples were labelled with Cy5. Hybridisations were performed with all 30 RNA samples, using Cy3-labeled chromosomal DNA of *A. terreus* as the reference.

The raw transcriptomics data were shown to be of high quality, based on visual inspection of the arrays after fluorescence scanning. Notably, also the hybridization with the partially degraded RNA samples gave good results.

The normalized data were subsequently combined. As the *A. terreus* array consisted out of two slides, different strategies of combining the data from the two slides were pursued, making use of the fact that the cDNA clones are present on both the A and B slide:

SET 1=mean expression signal of the cDNA clones on slide A and B, take only those spots that give a signal on both the A and B slide

SET 2=use only the signal of the cDNA spots on the A slide. Spots with a Signal/Background below 1.5 were removed.

SET 3=use only the signal of the cDNA spots on the B slide. Spots with a Signal/Background below 1.5 were removed.

SET 4=Combimean cDNA data of both the A and B slide;

i. If both measurement values were zero the combined value was zero;

ii. If both measurements values were both non-zero, the combined value was equal to the average of the two measurement values;

iii. If one of the two measurement values was zero and the other measurement value was non-zero, the combined value was equal to the non-zero measurement value.

SET 5=SET 1+normalized gDNA spots using the normalization factor calculated based on the cDNA clones.

The most relevant spots were subsequently identified by multivariate regression analysis. Multivariate data analysis (MVDA) tools seem very well suited to prioritize leads from functional genomics datasets. These tools take into account the inherent interdependency of biomolecules. These tools allow the identification of the specific genes that are the most important for a specific phenotype by determining the strength of the correlation of the expression of every gene with the biological question under study. Especially the regression tool partial least squares (PLS) holds great promise. Principally, the application of PLS results in a model (equation) that predicts a quantifiable phenotype of interest (e.g. itaconic acid titer, P) in terms of the transcripts (A, B, C, . . .) expressed in *A. terreus*;

$$P = b_1A + b_2B + b_3C + \dots$$

By subsequently ordering the transcripts based on the absolute value of the regression values (i.e. b_1, b_2, b_3, \dots) transcripts are identified that contribute the most to itaconate production.

PLS models with both the itaconate titers of the different samples and the itaconate productivity of the different samples were built using these different combined data sets. Moreover, not only linear models but also logarithmic models were built using the log of the itaconate titer (Table 4). Of these, only the (linear) itaconate titer models were reasonably good models as judged by the (double) cross validation results and the stability of these models (i.e. R^2 double validation ~0.4-0.5) (Table 4). The results of the other PLS models were very poor, and these models were not pursued.

TABLE 4

Overview of the PLS models build using the transcriptomics data set		
X (data set)	Y (Phenotype)	R^2 double cross validation PLS model
SET 1	Productivity	0.10
	Titer	0.51
	Log(titer)	0.05
SET 2	Productivity	0.13
	Titer	0.41
	Log(titer)	0.18
SET 3	Productivity	0.08
	Titer	0.45
	Log(titer)	0.06

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TABLE 4-continued

Overview of the PLS models build using the transcriptomics data set		
X (data set)	Y (Phenotype)	R ² double cross validation PLS model
SET 4	Productivity	0.07
	Titer	0.40
	Log(titer)	0.12
SET 5	Productivity	0.08
	Titer	0.38
	Log(titer)	0.05

Moreover, a second PLS model was built with the titer as the Y-variable, using only the transcripts whose regression value had an RSD <50% (as determined based on jack-knifing) in the first PLS model. This were, in general, only some 10-20% of the spots of the complete data set.

‘Top 20’-ies of the combined data data sets analyzed by PLS using the itaconic acid titer as the phenotype were generated. These ‘top-20’-ies were combined, and unique spots were identified (Table 5 and 6). In total 102 of the most relevant spots obtained after PLS analyses (based on 10 models; 5 data sets, 2 PLS models per data set) were selected for sequencing.

Of the selected spots, >92% were spots belonging to cDNA clones. However, also four of the 5 combined data sets contained only cDNA clones (see above).

Following sequence analysis of the 102 selected spots, the genes present on these inserts were identified by performing a homology search using BLAST based on the draft version of the *A. terreus* genome sequence as available from the BROAD institute (located on the World Wide Web at: broad.mit.edu/annotation/fgi/).

As different combined data sets/‘top 20’-ies were generated, the overall ranking of the transcripts, as reported in Table 5 was based on:

- (i) The frequency of occurrence of an individual spot in the top 20 of the different combined data sets analyzed

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- (ii) The sum of the overall rank of a spot in the different ‘top 20’-ies of the different combined data sets.

Table 5 shows the results of the genes identified on the 20 highest overall ranking spots identified by PLS analysis based on titer.

TABLE 5

Overall Top 20 PLS analysis - itaconic acid titer.				
Rank	Clone ID	Gene locus	Gene name	
1	AsTeR010H08			
2	AsTeR037H12			
3	AsTeR053F06			
4	AsTeR037C07			
5	AsTeR007H08			
6	AsTeR048G12			
7	AsTeR023B07			
8	AsTeR033F08			
9	AsTeR035E10			
10	AsTeR033A04			
11	AsTeR029F07			
12	AsTeR045A05			
13	AsTeR010H12			
14	AsTeR041C10			
15	AsTeR030D01	ATEG_09972.1	Predicted protein	
16	AsTeR009D10			
17	AsTeR032E02			
18	AsTeR032H04			
19	AsTeR004H04			
20	AsTeR054B06			

Moreover, a ranked list of the genes that were identified with the highest frequency amongst the in total 190 clones sequenced (i.e. 102 spots selected after PLS analyses and 88 spots obtained after the differential analyses—See EP 08151584) (Table 6).

TABLE 6

Most frequently identified genes amongst the 190 clones sequenced				
Freq.	Gene locus	# clones from differential approach	# clones from PLS approach	Regulation under itaconate producing conditions Gene name
25	ATEG_09970.1	25		Up mitochondrial tricarboxylic acid transporter - EP08151584
19				
15	ATEG_09971.1	14	1	Up cis-aconitate decarboxylase (EP 07112895)
14				
11				
7				
7				
4				
3				
3				
2	ATEG_09972.1		2	Up Predicted protein
2				
2				

TABLE 6-continued

Most frequently identified genes amongst the 190 clones sequenced				
Freq.	Gene locus	# clones from differential approach	# clones from PLS approach	Regulation under itaconate producing conditions
2				
2				
2				
2				
2				
2				

The ATEG_00972.1 gene, flanking cis-aconitate decarboxylase (ATEG_09971.1-EP 07112895), and the putative mitochondrial tricarboxylate transporter protein (ATEG_09970.1-EP08151584) were identified on two of the spots identified by PLS analysis (Table 6) and had an overall rank of 15 in the combined top 20 (Table 5). Just as the CAD gene and the MTAT gene, the ATEG_09972.1 gene, was found to be upregulated under itaconic acid producing environmental conditions.

lactor containing a zinc-finger domain (ATEG_09969.1). This gene was not identified using our transcriptomics approach, but considering its localization it is expected that it is relevant for itaconic acid synthesis FIG. 2 shows that also the lovas-tatin pathway genes are located on this cluster, suggesting a link between both pathways which are (mainly) specific for *A. terreus*.

Example 4

Homology Analysis of the ATEG_09972.1 Gene

A BLAST search was performed in order to identify homologous to the predicted protein ATEG_09972.1 (Table 7). High homologies were only found with genes from two other *A. terreus* strains. With other micro-organisms and more specifically fungi, homologues were found although with a relatively low homology. Based on the annotation of these homologous genes and the major facilitator superfamily domain identified in this gene, ATEG_09972.1 was identified as an itaconate exporter.

Example 5

(Co-)Expression of the ATEG_09972.1 Gene in *Aspergillus niger*

In order to unambiguously establish that the ATEG_09972.1 protein aids to the increased production of itaconic acid, a naturally non-itaconic acid producing fungal host was (co-)transformed with the CAD gene or transformed with the CAD and MTT (ATEG_09970.1) gene were co-transformed with the ATEG_09972.1 (MFS) gene.

Expression of the CAD (ATEG_09971.1) Gene in *Aspergillus niger*

TABLE 7

BLAST search results with ATEG_09972.1				
Rank	Protein	Best Hit	E value	Identity/ Similarity
1	Predicted protein	XP_001209274.1 <i>A. terreus</i>	0.0	100%/100%
2	unknown	AAD34564.1 <i>A. terreus</i>	0.0	92%/93%
3	Unnamed protein product	BAE57135.1 <i>A. oryzae</i>	2e-160	70%/84%
4	putitative MFS transporter	XP_749665.1 <i>A. fumigatus</i>	5e-135	64%/77%
5	putitative MFS transporter	XP_001260160.1 <i>N. fischeri</i>	5e-134	65%/79%
6	Hypothetical protein AN7512.2	XP_680781.1 <i>A. nidulans</i>	5e-123	59%/74%
7	Hypothetical protein AN6019.2	XP_663623.1 <i>A. nidulans</i>	1e-105	52%/68%
8	Unnamed protein product	BAE61268.1 <i>A. oryzae</i>	1e-91	45%/61%
9	pH-responsive protein 2 precursor	XP_001215904.1 <i>A. terreus</i>	2e-91	68%/81%
10	hypothetical protein Fgo2824.1	XP_383000.1 <i>G. zeae</i>	1e-81	47%/63%

It appears that at least the gene coding for the cis-aconitate decarboxylase (ATEG_09971.1) and the gene encoding the mitochondrial tricarboxylate transporter (ATEG_09970.1) lie in the same cluster in the *A. terreus* genome (FIG. 2).

A gene neighbouring CAD, the mitochondrial tricarboxylate transporter and the itaconate exporter is a putative regu-

A PCR generated copy of the gene encoding the CAD protein (see EP07112895) was generated. For this purpose two sets of primers were generated as shown below. PCR amplification based on *A. terreus* NRRL1960 genomic DNA resulted in the isolation of PCR fragments from which the complete coding region of the gene encoding the CAD protein, could be isolated as BspHI-BamHI fragments.

CAD full sequence 1529 bp

(SEQ ID NO: 11)

ORIGIN

(SEQ ID NO: 7)

BspHI cadfor40° C.

5'-ATCGTCATGACCAAGCAATCTG- 3'

(SEQ ID NO: 8)

BspHI cadfor53° C.

5'-ATCGTCATGACCAAGCAATCTGCGGACA- 3'

1 ATGACCAAGC AATCTGCGGA CAGCAACGCA AAGTCAGGAG TTACGTCCGA AATATGTCAT
61 TGGGCATCCA ACCTGGCCAC TGACGACATC CCTTCGGACG TATTAGAAAG AGCAAAATAC
121 CTTATTCTCG ACGGTATTGC ATGTGCCTGG GTTGGTGCAA GAGTGCCTTG GTCAGAGAAG
181 TATGTTTCAAG CAACGATGAG CTTTGAGCCG CCGGGGGCCT GCAGGGTGAT TGGATATGGA
241 CAGgtaaat ttattcactc tagacggtcc acaaagtata ctgacgatcc ttcgtataga
(intron)
301 AACTGGGGCC TGTTCAGCA GCCATGACCA ATTCCGCTTT CATAACGGCT ACGGAGCTTG
361 ACGACTACCA CAGCGAAGCC CCCCTACACT CTGCAAGCAT TGTCTTCCT GCGGTCTTTG
421 CAGCAAGTGA GGTCTTAGCC GAGCAGGCA AAACAATTC CGGTATAGAT GTTATTCTAG
481 CCGCCATTGT GGGGTTTGAA TCTGGCCAC GGATCGGCAA AGCAATCTAC GGATCGGACC
541 TCTTGAACAA CGGCTGGCAT TGTGGAGCTG TGTATGGCGC TCCAGCCGGT GCGCTGGCCA
601 CAGGAAAGCT CTTGCTCTA ACTCCAGACT CCATGGAAGA TGCTCTCGGA ATTGCGTGCA
661 CGCAAGCCTG TGGTTTAATG TCGGCGCAAT ACGGAGGCAT GGTAAGCGT GTGCAACACG
721 GATTTCGAGC GCGTAATGGT CTTCTTGGGG GACTGTTGGC CCATGGTGGG TACGAGGCAA
781 TGAAGGTGT CCTGGAGAGA TCTTACGCG GTTCTCTCAA GATGTTTACC AAGGGCAACG
841 GCAGAGAGCC TCCCTACAAA GAGGAGGAAG TGGTGGCTGG TCTCGTTTCA TTCTGGCATA
901 CCTTTACTAT TCGCATCAAG CTCTATGCCT GCTGCGGACT TGTCCATGGT CCAGTCGAGG
961 CTATCGAAAA CCTTCAGGGG AGATACCCCG AGCTCTTGAA TAGAGCCAAC CTCAGCAACA
1021 TTCGCCATGT TCATGTACAG CTTTCAACGG CTTCAACAG TCACTGTGGA TGGATACCAG
1081 AGGAGAGACC CATCAGTTCA ATCGCAGGGC AGATGAGTGT CGCATACATT CTCGCCGTCC
1141 AGCTGGTCGA CCAGCAATGT CTTTGTGCCC AGTTTCTGA GTTTGATGAC AACCTGGAGA
1201 GGCCAGAAAG TTGGGATCTG GCCAGGAAGG TTACTTCATC TCAAAGCGAA GAGTTTGATC
1261 AAGACGGCAA CTGTCTCAGT GCGGGTCGCG TGAGGATTGA GTTCAACGAT GGTCTTCTA
1321 TTACGGAAAG TGTCGAGAAG CCTCTTGGTG TCAAAGAGCC CATGCCAAAC GAACGGATTC
1381 TCCACAAATA CCGAACCCCT GCTGGTAGCG TGACGGACGA ATCCCGGGTG AAAGAGATTG
1441 AGGATCTTGT CCTCGGCCTG GACAGGCTCA CCGACATTAG CCCATTGCTG GAGCTGCTGA
1501 ATTGCCCCGT AAAATCGCCA CTGGTATAA

(SEQ ID NO: 9)

cadrev42° C. BamHI

3'-TTTAGCGGTGACCATATTCCTAGGCCCT- 5'

(SEQ ID NO: 10)

cadrev52° C. BamHI

3'-GGCATTTTAGCGGTGACCATATTCCTAGGCC- 5'

Translation of CAD Encoding Gene

Total amino acid number: 490, MW = 52710

(SEQ ID NO: 12)

1 M T K Q S A D S N A K S G V T S E I C H
21 W A S N L A T D D I P S D V L E R A K Y

-continued

41 L I L D G I A C A W V G A R V P W S E K
 61 Y V Q A T M S F E P P G A C R V I G Y G
 81 Q K L G P V A A A M T N S A F I Q A T E
 101 L D D Y H S E A P L H S A S I V L P A V
 121 F A A S E V L A E Q G K T I S G I D V I
 141 L A A I V G F E S G P R I G K A I Y G S
 161 D L L N N G W H C G A V Y G A P A G A L
 181 A T G K L F G L T P D S M E D A L G I A
 201 C T Q A C G L M S A Q Y G G M V K R V Q
 221 H G F A A R N G L L G G L L A H G G Y E
 241 A M K G V L E R S Y G G F L K M F T K G
 261 N G R E P P Y K E E E V V A G L G S F W
 281 H T F T I R I K L Y A C C G L V H G P V
 301 E A I E N L Q G R Y P E L L N R A N L S
 321 N I R H V H V Q L S T A S N S H C G W I
 341 P E E R P I S S I A G Q M S V A Y I L A
 361 V Q L V D Q Q C L L S Q F S E F D D N L
 381 E R P E V W D L A R K V T S S Q S E E F
 401 D Q D G N C L S A G R V R I E F N D G S
 421 S I T E S V E K P L G V K E P M P N E R
 441 I L H K Y R T L A G S V T D E S R V K E
 461 I E D L V L G L D R L T D I S P L L E L
 481 L N C P V K S P L V *

The resulting BspHI-BamHI fragment was cloned into the *Aspergillus* expression vector pAN52-4amdS derived from *Aspergillus* expression vector pAN52-4. The *Aspergillus* expression vector pAN52-4amdS was derived by cloning the *Aspergillus* selection marker amdS into the *Aspergillus* expression vector pAN52-4 (EMBL accession #Z32699).

Subsequently, an *Aspergillus niger* strain AB1.13 (Matern, I. E. et al., 1992, Mol. Gen. Genet. 234:332-336) was transformed with the CAD expression vector. AmdS transformants resulting for this experiment were purified by single colony purification and retested for their AmdS+ phenotype.

⁴⁰ Co-Expression of the CAD Gene and the ATEG 09970.1 Gene in *Aspergillus niger*

The ATEG_09970.1 gene (MTT) was synthesized (Gene-Art) and cloned into *Aspergillus niger* expression vector pAN52-5doubleNotI by restriction enzyme cutting sites of double NotI. The expression vector pAN52-5doubleNotI was derived by adding an extra NotI site in the *Aspergillus* expression vector pAN52-4 (EMBL accession #Z32699). Moreover, the codons of the clone were optimized for expression in the *Aspergillus niger* strain.

Translation of MTT cds (1-861) (SEQ ID NOS:13-14)

Universal code

Total amino acid number: 286, MW = 31503

Max ORF starts at AA pos 1 (may be DNA pos 1) for 286 AA (858 bases), MW = 31503

1 ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCTTTTTTGCGGCATTTTGCCTTCCT
1 M S I Q H F R V A L I P F F A A F C L P

61 GTTTTGTCTCACCCAGAACGCTGGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCA
21 V F A H P E T L V K V K D A E D Q L G A

121 CGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTGCCCCC
41 R V G Y I E L D L N S G K I L E S F R P

181 GAAGAAGCTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCC
61 E E R F P M M S T F K V L L C G A V L S

-continued

241 CGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGATACACTATTCTCAGAATGACTTG
81 R I D A G Q E Q L G R R I H Y S Q N D L

301 GTTGAGTACTACCCAGTACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTA
101 V E Y S P V T E K H L T D G M T V R E L

361 TGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATC
121 C S A A I T M S D N T A A N L L L T T I

421 GGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACCTCGCCTT
141 G G P K E L T A F L H N M G D H V T R L

481 GATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATG
161 D R W E P E L N E A I P N D E R D T T M

541 CCTGTAGCAATGGCAACAACGTTGCGCAAACCTATTAACCTGGCGAACTACTTACTCTAGCT
181 P V A M A T T L R K L L T G E L L T L A

601 TCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGC
201 S R Q Q L I D W M E A D K V A G P L L R

661 TCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCT
221 S A L P A G W F I A D K S G A G E R G S

721 CGCGGTATCATTCGAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTAC
241 R G I I A A L G P D G K P S R I V V I Y

781 ACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCC
261 T T G S Q A T M D E R N R Q I A E I G A

841 TCACTGATTAAGCATTGGTAA
281 S L I K H W *

Subsequently, an *Aspergillus niger* strain AB1.13 (Mat-
tern, I. E. et al., 1992, Mol. Gen. Genet. 234:332-336) was
co-transformed with the CAD expression vector and the MTT
expression vector. AmdS transformants resulting for this
experiment were purified by single colony purification and
retested for their AmdS⁺ phenotype.
Co-Expression of the CAD Gene, MTT Gene
(ATEG_09970.1) Together with the ATEG-09972.1 Gene in
Aspergillus niger

The ATEG-09972.1 (MFS) gene was synthesized (Gene-
Art) and cloned into *Aspergillus niger* expression vector
pAN52-5doubleNotI by restriction enzyme cutting sites of
double NotI. The expression vector pAN52-5doubleNotI was
derived by adding an extra NotI site in the *Aspergillus* expres-
sion vector pAN52-4 (EMBL accession #Z32699). More-
over, codons of the clone were optimized for expression in the
Aspergillus niger strain.

Subsequently, an *Aspergillus niger* strain AB1.13 (Mat-
tern, I. E. et al., 1992, Mol. Gen. Genet. 234:332-336) was
co-transformed with the CAD expression vector, the MTT
expression vector and the MFS expression vector. AmdS
transformants resulting for this experiment were purified by
single colony purification and retested for their AmdS⁺ phe-
notype.

Analysis of *A. niger* Transformants for Itaconic Acid Produc-
tion

Several positive transformants and the parental host strain
were subsequently cultured in Shake Flask in MM medium
supplied with uridine containing glucose as C-source and
nitrate as N-source. Medium samples from the various cul-
tures were analyzed by HPLC for the presence of itaconic
acid (Table 8).

Shake Flask Medium Compositions:

Per litre: 0.52 g of KCl, 2.4 g of NaNO₃, 1.56 g of KH₂PO₄,
0.24 g of MgSO₄*7H₂O, 5 mg of Fe(III)SO₄*7H₂O, 5 mg of
MnCl₂*4H₂O, 0.022 g of ZnSO₄*7H₂O, 0.011 g of H₃BO₃,
1.7 mg of CoCl₂*6H₂O and 2.44 g of uridine, 100 g of glucose
as a carbon source. All media were prepared in demineralised
water.

HPLC analysis was performed with a reversed phase col-
umn, using a Develosil™ 3 µm RP-Aqueous C30 140A col-
umn at a constant temperature of 25° C., with elution with 20
mM NaH₂PO₄, pH 2.25 and acetonitril. Compounds were
detected by UV at 210 nm using a Waters 2487 Dual wave-
length Absorbance detector (Milford, Mass., USA). Reten-
tion time of itaconic acid was 18.82 min.

TABLE 8

Itaconic acid concentration in the culture fluid of the
A. niger AB1.13 transformants cultivated in shake flasks.
Aspergillus niger AB 1.13 transformants (AB 1.13 CAD)

strain	code	time (hrs)	itaconic acid mg/g wet weight
AB 1.13	WT	54	0
AB 1.13 CAD	5.1	54	1.0
AB 1.13 CAD	7.2	54	0.7
AB 1.13 CAD	10.1	54	1.4
AB 1.13 CAD	14.2	54	1.2
AB 1.13 CAD	16.1	54	1.2
AB 1.13 CAD + MTT	4.1	54	1.3
AB 1.13 CAD + MTT	6.2	54	1.5
AB 1.13 CAD + MTT	2.2.1	54	2.2
AB 1.13 CAD + MTT + MFS	9.2.1*	54	2.3
AB 1.13 CAD + MTT + MFS	9.2.2*	54	2.5
AB 1.13 CAD + MTT + MFS	9.4.1*	54	2.5
AB 1.13 CAD + MTT + MFS	12.1.1	54	2.3

*Duplicate isolates of the same transformant.

No itaconic acid was detected in the supernatant of the
parental strain while in the culture fluid of the strains contain-
ing the CAD gene (strains marked CAD), itaconic acid was
detected.

In both the culture fluid of the strains containing the CAD
gene and the strains containing both the CAD gene and MTT
gene (strains marked CAD+MTT) and the strains containing
the CAD, the MTT and the MFS gene (strains marked CAD+
MTT+MFS), itaconic acid was detected (Table 8). In all MFS

expressing strains more itaconic acid was produced in the culture fluid than in the strains expressing only the CAD gene, or the CAD and the MTT gene. Moreover, the average itaconic acid concentration was higher in the culture fluid of the strains expressing the MFS, the CAD and the MTT gene

compared to the transformants expressing only the CAD or the CAD+MTT gene: 2.4 mg itaconic acid/g mycelial wet weight versus 1.1 mg itaconic acid/g mycelial wet weight (CAD gene only) and 1.7 mg itaconic acid/g mycelial wet weight (CAD+MTT gene—Table 8).

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 14

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<212> TYPE: DNA

<213> ORGANISM: *Aspergillus terreus*

<400> SEQUENCE: 1

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cctgaaatcg cgaatgaatt tgatatgact gtcgagacta tcaacatctc caatgctggt    240
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tggggctcgt gctttctctg ctatttttcc cgaaaatcga aggaaattct gagaaggctc    780
caacggcggt taaaccgacc acacttgtea caatcatatc gaaattctcc ccaacggatg    840
tgctcaagca gtgggtgtat ccaaatgtct ttcttgccgt aagtgtctgg gacatatacc    900
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aagcgcggat tccgtctccc tcaggatcga ctccacagcg ggctcatcac attgttcgcc    1200
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gtagtgccea taatcgcggc gttcttcgcg ggctgggggc tcatgggcag ttttaactgc    1320
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<211> LENGTH: 1212

<212> TYPE: DNA

<213> ORGANISM: *Aspergillus terreus*

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1212)

<400> SEQUENCE: 2

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ggt agc gga caa aac gag cca gag aaa aag ggc cgt gat att cca tta	96
Gly Ser Gly Gln Asn Glu Pro Glu Lys Lys Gly Arg Asp Ile Pro Leu	
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tgg aga aaa tgt gtc att acg ttt gtt gtt agt tgg atg act cta gtc	144
Trp Arg Lys Cys Val Ile Thr Phe Val Val Ser Trp Met Thr Leu Val	
35 40 45	
gtt act ttc tcc agt act tgt ctt ctt cct gcc gcc cct gaa atc gcg	192
Val Thr Phe Ser Ser Thr Cys Leu Leu Pro Ala Ala Pro Glu Ile Ala	
50 55 60	
aat gaa ttt gat atg act gtc gag act atc aac atc tcc aat gct ggt	240
Asn Glu Phe Asp Met Thr Val Glu Thr Ile Asn Ile Ser Asn Ala Gly	
65 70 75 80	
gtc cta gtt gcc atg gga tat tca tcc ctc ata tgg ggt ccc atg aac	288
Val Leu Val Ala Met Gly Tyr Ser Ser Leu Ile Trp Gly Pro Met Asn	
85 90 95	
aag tta gtc ggc cgg cgg aca tca tac aat ctg gcc att tca atg ctt	336
Lys Leu Val Gly Arg Thr Ser Tyr Asn Leu Ala Ile Ser Met Leu	
100 105 110	
tgt gca tgc tcc gct gga acg gca gcg gcg ata aac gag gaa atg ttc	384
Cys Ala Cys Ser Ala Gly Thr Ala Ala Ala Ile Asn Glu Glu Met Phe	
115 120 125	
ata gcg ttc aga gtg ttg agc ggc tta acc gga acc tcg ttc atg gtc	432
Ile Ala Phe Arg Val Leu Ser Gly Leu Thr Gly Thr Ser Phe Met Val	
130 135 140	
tca ggc caa act gtt ctt gca gat atc ttt gag cct gtt tac cgt ggg	480
Ser Gly Gln Thr Val Leu Ala Asp Ile Phe Glu Pro Val Tyr Arg Gly	
145 150 155 160	
acg gcc gta ggt ttc ttc atg gcc ggg act ctt tct ggc cct gca ata	528
Thr Ala Val Gly Phe Phe Met Ala Gly Thr Leu Ser Gly Pro Ala Ile	
165 170 175	
ggc ccc tgc gtg gga ggg gtc atc gtc act ttc acg agt tgg cgt gtt	576
Gly Pro Cys Val Gly Gly Val Ile Val Thr Phe Thr Ser Trp Arg Val	
180 185 190	
atc ttc tgg ctt caa cta ggt atg agc ggg ctg ggg ctc gtg ctt tct	624
Ile Phe Trp Leu Gln Leu Gly Met Ser Gly Leu Gly Leu Val Leu Ser	
195 200 205	
ctg cta ttt ttc ccg aaa atc gaa gga aat tct gag aag gtc tca acg	672
Leu Leu Phe Phe Pro Lys Ile Glu Gly Asn Ser Glu Lys Val Ser Thr	
210 215 220	
gcg ttt aaa ccg acc aca ctt gtc aca atc ata tcg aaa ttc tcc cca	720
Ala Phe Lys Pro Thr Leu Val Thr Ile Ile Ser Lys Phe Ser Pro	
225 230 235 240	
acg gat gtg ctc aag cag tgg gtg tat cca aat gtc ttt ctt gcc gac	768
Thr Asp Val Leu Lys Gln Trp Val Tyr Pro Asn Val Phe Leu Ala Asp	
245 250 255	
tta tgc tgt ggc ctc ctg gca atc acg caa tat tcg atc ctg act tca	816
Leu Cys Cys Gly Leu Leu Ala Ile Thr Gln Tyr Ser Ile Leu Thr Ser	
260 265 270	
gct cgt gcc ata ttc aac tca cga ttt cat tta acg act gcc cta gta	864
Ala Arg Ala Ile Phe Asn Ser Arg Phe His Leu Thr Thr Ala Leu Val	
275 280 285	
tcg ggt ctc ttc tac ctc gct cca ggt gcc ggg ttc ctg ata ggc agt	912
Ser Gly Leu Phe Tyr Leu Ala Pro Gly Ala Gly Phe Leu Ile Gly Ser	
290 295 300	
ctc gtc ggc ggt aaa ctt tcg gat cgc acc gtt cgg aga tac ata gta	960
Leu Val Gly Gly Lys Leu Ser Asp Arg Thr Val Arg Arg Tyr Ile Val	
305 310 315 320	
aag cgc gga ttc cgt ctc cct cag gat cga ctc cac agc ggg ctc atc	1008
Lys Arg Gly Phe Arg Leu Pro Gln Asp Arg Leu His Ser Gly Leu Ile	

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325	330	335	
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Thr Leu Phe Ala Val Leu Pro Ala Gly Thr Leu Ile Tyr Gly Trp Thr			
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ctc caa gag gat aag ggt gat atg gta gtg ccc ata atc gcg gcg ttc			1104
Leu Gln Glu Asp Lys Gly Asp Met Val Val Pro Ile Ile Ala Ala Phe			
355	360	365	
ttc gcg gcc tgg ggg ctc atg ggc agt ttt aac tgc ctg aac act tac			1152
Phe Ala Gly Trp Gly Leu Met Gly Ser Phe Asn Cys Leu Asn Thr Tyr			
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gtg gct ggt ttg ttc cac acc ctc att tat cta ttc cct ttg tgt aca			1200
Val Ala Gly Leu Phe His Thr Leu Ile Tyr Leu Phe Pro Leu Cys Thr			
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<210> SEQ ID NO 3

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<212> TYPE: PRT

<213> ORGANISM: Aspergillus terreus

<400> SEQUENCE: 3

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20 25 30

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35 40 45

Val Thr Phe Ser Ser Thr Cys Leu Leu Pro Ala Ala Pro Glu Ile Ala
50 55 60

Asn Glu Phe Asp Met Thr Val Glu Thr Ile Asn Ile Ser Asn Ala Gly
65 70 75 80

Val Leu Val Ala Met Gly Tyr Ser Ser Leu Ile Trp Gly Pro Met Asn
85 90 95

Lys Leu Val Gly Arg Arg Thr Ser Tyr Asn Leu Ala Ile Ser Met Leu
100 105 110

Cys Ala Cys Ser Ala Gly Thr Ala Ala Ala Ile Asn Glu Glu Met Phe
115 120 125

Ile Ala Phe Arg Val Leu Ser Gly Leu Thr Gly Thr Ser Phe Met Val
130 135 140

Ser Gly Gln Thr Val Leu Ala Asp Ile Phe Glu Pro Val Tyr Arg Gly
145 150 155 160

Thr Ala Val Gly Phe Phe Met Ala Gly Thr Leu Ser Gly Pro Ala Ile
165 170 175

Gly Pro Cys Val Gly Gly Val Ile Val Thr Phe Thr Ser Trp Arg Val
180 185 190

Ile Phe Trp Leu Gln Leu Gly Met Ser Gly Leu Gly Leu Val Leu Ser
195 200 205

Leu Leu Phe Phe Pro Lys Ile Glu Gly Asn Ser Glu Lys Val Ser Thr
210 215 220

Ala Phe Lys Pro Thr Thr Leu Val Thr Ile Ile Ser Lys Phe Ser Pro
225 230 235 240

Thr Asp Val Leu Lys Gln Trp Val Tyr Pro Asn Val Phe Leu Ala Asp
245 250 255

Leu Cys Cys Gly Leu Leu Ala Ile Thr Gln Tyr Ser Ile Leu Thr Ser
260 265 270

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Ala Arg Ala Ile Phe Asn Ser Arg Phe His Leu Thr Thr Ala Leu Val
 275 280 285

Ser Gly Leu Phe Tyr Leu Ala Pro Gly Ala Gly Phe Leu Ile Gly Ser
 290 295 300

Leu Val Gly Gly Lys Leu Ser Asp Arg Thr Val Arg Arg Tyr Ile Val
 305 310 315 320

Lys Arg Gly Phe Arg Leu Pro Gln Asp Arg Leu His Ser Gly Leu Ile
 325 330 335

Thr Leu Phe Ala Val Leu Pro Ala Gly Thr Leu Ile Tyr Gly Trp Thr
 340 345 350

Leu Gln Glu Asp Lys Gly Asp Met Val Val Pro Ile Ile Ala Ala Phe
 355 360 365

Phe Ala Gly Trp Gly Leu Met Gly Ser Phe Asn Cys Leu Asn Thr Tyr
 370 375 380

Val Ala Gly Leu Phe His Thr Leu Ile Tyr Leu Phe Pro Leu Cys Thr
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Cys Pro Gln

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 <212> TYPE: DNA
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cttctgcaa ccccgagat cgcgaggag ttcaacacca cactgagac cctcaacatc    240
accaatgcgc gegttttgcg ggcattgggc ttctcgtcgc ttatctggg tcccttgaat    300
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gcagcgacgg gggctgcagt agacttgaag atgtttacgg cttttcagat gttgagcggg    420
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aatcaaaaca ggaatccaaa gaggaaccgg aagaaaaaga gaagaggaca gtactttccg    780
ccctacgcct cttcaatccc ctccgaatct tcagacaatg ggtctatccc aacgtcttct    840
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gacctacccg tccgaagta catcgctcgt cgcggtcttc gattgcccc ggatcgctc   1140
aactccggcc tcgtcacctt gttcgcgtg ctaccggtt cggcgctgat ctacggtgg   1200
accctgcagg aggagaaggg tggtatggc gtgccgattt tggcgcggtt ttttgacgg   1260
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<212> TYPE: DNA
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<220> FEATURE:
<221> NAME/KEY: CDS
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<400> SEQUENCE: 5

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gcc acg aaa gag aag gaa gag aaa ggc agc aaa gtt gaa aag ggt tac 96
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ggt ctt cct ttg tgg cgg aaa tgt atc atc ctc ttc gtc gtc agt tgg 144
Gly Leu Pro Leu Trp Arg Lys Cys Ile Ile Leu Phe Val Val Ser Trp
35 40 45

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Met Thr Leu Ala Val Thr Phe Ser Ser Thr Ser Leu Leu Pro Ala Thr
50 55 60

ccc gag atc gcc gag gag ttc aac acc acc act gag acc ctc aac atc 240
Pro Glu Ile Ala Glu Glu Phe Asn Thr Thr Thr Glu Thr Leu Asn Ile
65 70 75 80

acc aat gcc ggc gtt ttg ctg gct atg ggc ttc tcg tcg ctt atc tgg 288
Thr Asn Ala Gly Val Leu Leu Ala Met Gly Phe Ser Ser Leu Ile Trp
85 90 95

ggt ccc ttg aat aat ctg att gga aga agg ctc tcg tat aac att gcg 336
Gly Pro Leu Asn Asn Leu Ile Gly Arg Arg Leu Ser Tyr Asn Ile Ala
100 105 110

atc ttc atg ctc tgt gtg tgt tcg gca gcg acg ggg gct gca gta gac 384
Ile Phe Met Leu Cys Val Cys Ser Ala Ala Thr Gly Ala Ala Val Asp
115 120 125

ttg aag atg ttt acg gct ttt cga gtg ttg agc ggt ttg acg ggg acg 432
Leu Lys Met Phe Thr Ala Phe Arg Val Leu Ser Gly Leu Thr Gly Thr
130 135 140

tca ttc atg gta tcg gga cag acc att ctg gcg gac att ttt gaa ccg 480
Ser Phe Met Val Ser Gly Gln Thr Ile Leu Ala Asp Ile Phe Glu Pro
145 150 155 160

gtt gtc cgt ggt aca gcc gtg gga ttc ttt atg gct gga tct gtc tcc 528
Val Val Arg Gly Thr Ala Val Gly Phe Phe Met Ala Gly Ser Val Ser
165 170 175

ggt cct gca att ggg ccc tgt atc gga ggc ctc atc gtc acc ttc tcc 576
Gly Pro Ala Ile Gly Pro Cys Ile Gly Gly Leu Ile Val Thr Phe Ser
180 185 190

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Glu Glu Pro Glu Glu Lys Glu Lys Arg Thr Val Leu Ser Ala Leu Arg			
225	230	235	240
ctc ttc aat ccc ctc cga atc ttc aga caa tgg gtc tat ccc aac gtc			768
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245	250	255	
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Phe Phe Ser Asp Leu Thr Cys Gly Leu Leu Ala Thr Phe Gln Tyr Ser			
260	265	270	
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Leu Leu Thr Ser Ala Arg Ser Ile Phe Asn Pro Arg Phe His Leu Thr			
275	280	285	
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Thr Ala Leu Ile Ser Gly Leu Phe Tyr Leu Ala Pro Gly Ala Gly Phe			
290	295	300	
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Leu Ile Gly Ser Ile Ile Gly Gly Lys Leu Ser Asp Arg Thr Val Arg			
305	310	315	320
aag tac atc gtc cgt cgc ggc ttc cga ttg ccc cag gat cgc ctc aac			1008
Lys Tyr Ile Val Arg Arg Gly Phe Arg Leu Pro Gln Asp Arg Leu Asn			
325	330	335	
tcc ggc ctc gtc acc ctg ttc gcc gtg cta ccc gtt tcg gcg ctg atc			1056
Ser Gly Leu Val Thr Leu Phe Ala Val Leu Pro Val Ser Ala Leu Ile			
340	345	350	
tac ggc tgg acc ctg cag gag gag aag ggt ggt atg gtc gtg ccg att			1104
Tyr Gly Trp Thr Leu Gln Glu Glu Lys Gly Gly Met Val Val Pro Ile			
355	360	365	
ttg gcg gcg ttt ttt gca ggt tgg ggg ctt atg ggc agt ttt aat act			1152
Leu Ala Ala Phe Phe Ala Gly Trp Gly Leu Met Gly Ser Phe Asn Thr			
370	375	380	
ttg aac act tat gtt gct gag gct ctg ccg cat aag cgc tcc gaa gtc			1200
Leu Asn Thr Tyr Val Ala Glu Ala Leu Pro His Lys Arg Ser Glu Val			
385	390	395	400
atc gct gga aag tat atc atc cag tat atc ttt tcg gcg ggg agt agt			1248
Ile Ala Gly Lys Tyr Ile Ile Gln Tyr Ile Phe Ser Ala Gly Ser Ser			
405	410	415	
gcg ctt gtg gtg ccg att att aat gcc att ggg gtt ggg tgg act ttt			1296
Ala Leu Val Val Pro Ile Ile Asn Ala Ile Gly Val Gly Trp Thr Phe			
420	425	430	
acc att tgt gtg atc ttt tcc atc atc ggt ggt ctg tta acg atg gct			1344
Thr Ile Cys Val Ile Phe Ser Ile Ile Gly Gly Leu Leu Thr Met Ala			
435	440	445	
acc gcg cga tgg ggt ctg gat atg caa caa tgg gtg gag agg aag ttc			1392
Thr Ala Arg Trp Gly Leu Asp Met Gln Gln Trp Val Glu Arg Lys Phe			
450	455	460	
cgc att cat gat aaa cca ggg ttt tga			1419
Arg Ile His Asp Lys Pro Gly Phe			
465	470		

<210> SEQ ID NO 6

<211> LENGTH: 472

<212> TYPE: PRT

<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 6

Met Gly Gln Pro Asp Leu Glu Ser Gln Thr Pro Lys Thr Ile Asp Gly

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1	5	10	15
Ala Thr Lys Glu Lys Glu Glu Lys Gly Ser Lys Val Glu Lys Gly Tyr	20	25	30
Gly Leu Pro Leu Trp Arg Lys Cys Ile Ile Leu Phe Val Val Ser Trp	35	40	45
Met Thr Leu Ala Val Thr Phe Ser Ser Thr Ser Leu Leu Pro Ala Thr	50	55	60
Pro Glu Ile Ala Glu Glu Phe Asn Thr Thr Thr Glu Thr Leu Asn Ile	65	70	75
Thr Asn Ala Gly Val Leu Leu Ala Met Gly Phe Ser Ser Leu Ile Trp	85	90	95
Gly Pro Leu Asn Asn Leu Ile Gly Arg Arg Leu Ser Tyr Asn Ile Ala	100	105	110
Ile Phe Met Leu Cys Val Cys Ser Ala Ala Thr Gly Ala Ala Val Asp	115	120	125
Leu Lys Met Phe Thr Ala Phe Arg Val Leu Ser Gly Leu Thr Gly Thr	130	135	140
Ser Phe Met Val Ser Gly Gln Thr Ile Leu Ala Asp Ile Phe Glu Pro	145	150	155
Val Val Arg Gly Thr Ala Val Gly Phe Phe Met Ala Gly Ser Val Ser	165	170	175
Gly Pro Ala Ile Gly Pro Cys Ile Gly Gly Leu Ile Val Thr Phe Ser	180	185	190
Ser Trp Arg Asn Ile Tyr Trp Leu Gln Val Gly Met Thr Gly Phe Gly	195	200	205
Leu Val Leu Ala Ile Leu Phe Val Pro Glu Ile Lys Gln Glu Ser Lys	210	215	220
Glu Glu Pro Glu Glu Lys Glu Lys Arg Thr Val Leu Ser Ala Leu Arg	225	230	235
Leu Phe Asn Pro Leu Arg Ile Phe Arg Gln Trp Val Tyr Pro Asn Val	245	250	255
Phe Phe Ser Asp Leu Thr Cys Gly Leu Leu Ala Thr Phe Gln Tyr Ser	260	265	270
Leu Leu Thr Ser Ala Arg Ser Ile Phe Asn Pro Arg Phe His Leu Thr	275	280	285
Thr Ala Leu Ile Ser Gly Leu Phe Tyr Leu Ala Pro Gly Ala Gly Phe	290	295	300
Leu Ile Gly Ser Ile Ile Gly Gly Lys Leu Ser Asp Arg Thr Val Arg	305	310	315
Lys Tyr Ile Val Arg Arg Gly Phe Arg Leu Pro Gln Asp Arg Leu Asn	325	330	335
Ser Gly Leu Val Thr Leu Phe Ala Val Leu Pro Val Ser Ala Leu Ile	340	345	350
Tyr Gly Trp Thr Leu Gln Glu Glu Lys Gly Gly Met Val Val Pro Ile	355	360	365
Leu Ala Ala Phe Phe Ala Gly Trp Gly Leu Met Gly Ser Phe Asn Thr	370	375	380
Leu Asn Thr Tyr Val Ala Glu Ala Leu Pro His Lys Arg Ser Glu Val	385	390	395
Ile Ala Gly Lys Tyr Ile Ile Gln Tyr Ile Phe Ser Ala Gly Ser Ser	405	410	415
Ala Leu Val Val Pro Ile Ile Asn Ala Ile Gly Val Gly Trp Thr Phe	420	425	430

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Thr Ile Cys Val Ile Phe Ser Ile Ile Gly Gly Leu Leu Thr Met Ala
 435 440 445

Thr Ala Arg Trp Gly Leu Asp Met Gln Gln Trp Val Glu Arg Lys Phe
 450 455 460

Arg Ile His Asp Lys Pro Gly Phe
 465 470

<210> SEQ ID NO 7
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 7

atcgatcatga ccaagcaatc tg 22

<210> SEQ ID NO 8
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 8

atcgatcatga ccaagcaatc tgcggaca 28

<210> SEQ ID NO 9
 <211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 9

ttagcggtg accatattcc taggcct 28

<210> SEQ ID NO 10
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: primer

<400> SEQUENCE: 10

ggcatttttag cggtgaccat attcctaggc ccc 33

<210> SEQ ID NO 11
 <211> LENGTH: 1529
 <212> TYPE: DNA
 <213> ORGANISM: Aspergillus terreus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(243)
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (300)..(1526)

<400> SEQUENCE: 11

atg acc aag caa tct gcg gac agc aac gca aag tca gga gtt acg tcc 48
 Met Thr Lys Gln Ser Ala Asp Ser Asn Ala Lys Ser Gly Val Thr Ser
 1 5 10 15

gaa ata tgt cat tgg gca tcc aac ctg gcc act gac gac atc cct tcg 96
 Glu Ile Cys His Trp Ala Ser Asn Leu Ala Thr Asp Asp Ile Pro Ser
 20 25 30

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gac gta tta gaa aga gca aaa tac ctt att ctc gac ggt att gca tgt Asp Val Leu Glu Arg Ala Lys Tyr Leu Ile Leu Asp Gly Ile Ala Cys 35 40 45	144
gcc tgg gtt ggt gca aga gtg cct tgg tca gag aag tat gtt cag gca Ala Trp Val Gly Ala Arg Val Pro Trp Ser Glu Lys Tyr Val Gln Ala 50 55 60	192
acg atg agc ttt gag ccg ccg ggg gcc tgc agg gtg att gga tat gga Thr Met Ser Phe Glu Pro Pro Gly Ala Cys Arg Val Ile Gly Tyr Gly 65 70 75 80	240
cag gtaaaatttta ttcaactctag acggtccaca aagtatactg acgatccttc gtatag Gln	299
aaa ctg ggg cct gtt gca gca gcc atg acc aat tcc gct ttc ata cag Lys Leu Gly Pro Val Ala Ala Ala Met Thr Asn Ser Ala Phe Ile Gln 85 90 95	347
gct acg gag ctt gac gac tac cac agc gaa gcc ccc cta cac tct gca Ala Thr Glu Leu Asp Asp Tyr His Ser Glu Ala Pro Leu His Ser Ala 100 105 110	395
agc att gtc ctt cct gcg gtc ttt gca gca agt gag gtc tta gcc gag Ser Ile Val Leu Pro Ala Val Phe Ala Ala Ser Glu Val Leu Ala Glu 115 120 125	443
cag ggc aaa aca att tcc ggt ata gat gtt att cta gcc gcc att gtg Gln Gly Lys Thr Ile Ser Gly Ile Asp Val Ile Leu Ala Ala Ile Val 130 135 140 145	491
ggg ttt gaa tct ggc cca cgg atc ggc aaa gca atc tac gga tcg gac Gly Phe Glu Ser Gly Pro Arg Ile Gly Lys Ala Ile Tyr Gly Ser Asp 150 155 160	539
ctc ttg aac aac ggc tgg cat tgt gga gct gtg tat ggc gct cca gcc Leu Leu Asn Asn Gly Trp His Cys Gly Ala Val Tyr Gly Ala Pro Ala 165 170 175	587
ggt gcg ctg gcc aca gga aag ctc ttc ggt cta act cca gac tcc atg Gly Ala Leu Ala Thr Gly Lys Leu Phe Gly Leu Thr Pro Asp Ser Met 180 185 190	635
gaa gat gct ctc gga att gcg tgc acg caa gcc tgt ggt tta atg tcg Glu Asp Ala Leu Gly Ile Ala Cys Thr Gln Ala Cys Gly Leu Met Ser 195 200 205	683
gcg caa tac gga ggc atg gta aag cgt gtg caa cac gga ttc gca gcg Ala Gln Tyr Gly Gly Met Val Lys Arg Val Gln His Gly Phe Ala Ala 210 215 220 225	731
cgt aat ggt ctt ctt ggg gga ctg ttg gcc cat ggt ggg tac gag gca Arg Asn Gly Leu Leu Gly Gly Leu Leu Ala His Gly Gly Tyr Glu Ala 230 235 240	779
atg aaa ggt gtc ctg gag aga tct tac ggc ggt ttc ctc aag atg ttc Met Lys Gly Val Leu Glu Arg Ser Tyr Gly Gly Phe Leu Lys Met Phe 245 250 255	827
acc aag ggc aac ggc aga gag cct ccc tac aaa gag gag gaa gtg gtg Thr Lys Gly Asn Gly Arg Glu Pro Pro Tyr Lys Glu Glu Glu Val Val 260 265 270	875
gct ggt ctc ggt tca ttc tgg cat acc ttt act att cgc atc aag ctc Ala Gly Leu Gly Ser Phe Trp His Thr Phe Thr Ile Arg Ile Lys Leu 275 280 285	923
tat gcc tgc tgc gga ctt gtc cat ggt cca gtc gag gct atc gaa aac Tyr Ala Cys Cys Gly Leu Val His Gly Pro Val Glu Ala Ile Glu Asn 290 295 300 305	971
ctt cag ggg aga tac ccc gag ctc ttg aat aga gcc aac ctc agc aac Leu Gln Gly Arg Tyr Pro Glu Leu Leu Asn Arg Ala Asn Leu Ser Asn 310 315 320	1019
att cgc cat gtt cat gta cag ctt tca acg gct tcg aac agt cac tgt Ile Arg His Val His Val Gln Leu Ser Thr Ala Ser Asn Ser His Cys 325 330 335	1067

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gga tgg ata cca gag gag aga ccc atc agt tca atc gca ggg cag atg	1115
Gly Trp Ile Pro Glu Glu Arg Pro Ile Ser Ser Ile Ala Gly Gln Met	
340 345 350	
agt gtc gca tac att ctc gcc gtc cag ctg gtc gac cag caa tgt ctt	1163
Ser Val Ala Tyr Ile Leu Ala Val Gln Leu Val Asp Gln Gln Cys Leu	
355 360 365	
ttg tcc cag ttt tct gag ttt gat gac aac ctg gag agg cca gaa gtt	1211
Leu Ser Gln Phe Ser Glu Phe Asp Asp Asn Leu Glu Arg Pro Glu Val	
370 375 380 385	
tgg gat ctg gcc agg aag gtt act tca tct caa agc gaa gag ttt gat	1259
Trp Asp Leu Ala Arg Lys Val Thr Ser Ser Gln Ser Glu Glu Phe Asp	
390 395 400	
caa gac ggc aac tgt ctc agt gcg ggt cgc gtg agg att gag ttc aac	1307
Gln Asp Gly Asn Cys Leu Ser Ala Gly Arg Val Arg Ile Glu Phe Asn	
405 410 415	
gat ggt tct tct att acg gaa agt gtc gag aag cct ctt ggt gtc aaa	1355
Asp Gly Ser Ser Ile Thr Glu Ser Val Glu Lys Pro Leu Gly Val Lys	
420 425 430	
gag ccc atg cca aac gaa cgg att ctc cac aaa tac cga acc ctt gct	1403
Glu Pro Met Pro Asn Glu Arg Ile Leu His Lys Tyr Arg Thr Leu Ala	
435 440 445	
ggt agc gtg acg gac gaa tcc cgg gtg aaa gag att gag gat ctt gtc	1451
Gly Ser Val Thr Asp Glu Ser Arg Val Lys Glu Ile Glu Asp Leu Val	
450 455 460 465	
ctc ggc ctg gac agg ctc acc gac att agc cca ttg ctg gag ctg ctg	1499
Leu Gly Leu Asp Arg Leu Thr Asp Ile Ser Pro Leu Leu Glu Leu Leu	
470 475 480	
aat tgc ccc gta aaa tcg cca ctg gta taa	1529
Asn Cys Pro Val Lys Ser Pro Leu Val	
485 490	

<210> SEQ ID NO 12

<211> LENGTH: 490

<212> TYPE: PRT

<213> ORGANISM: Aspergillus terreus

<400> SEQUENCE: 12

Met Thr Lys Gln Ser Ala Asp Ser Asn Ala Lys Ser Gly Val Thr Ser	
1 5 10 15	
Glu Ile Cys His Trp Ala Ser Asn Leu Ala Thr Asp Asp Ile Pro Ser	
20 25 30	
Asp Val Leu Glu Arg Ala Lys Tyr Leu Ile Leu Asp Gly Ile Ala Cys	
35 40 45	
Ala Trp Val Gly Ala Arg Val Pro Trp Ser Glu Lys Tyr Val Gln Ala	
50 55 60	
Thr Met Ser Phe Glu Pro Pro Gly Ala Cys Arg Val Ile Gly Tyr Gly	
65 70 75 80	
Gln Lys Leu Gly Pro Val Ala Ala Ala Met Thr Asn Ser Ala Phe Ile	
85 90 95	
Gln Ala Thr Glu Leu Asp Asp Tyr His Ser Glu Ala Pro Leu His Ser	
100 105 110	
Ala Ser Ile Val Leu Pro Ala Val Phe Ala Ala Ser Glu Val Leu Ala	
115 120 125	
Glu Gln Gly Lys Thr Ile Ser Gly Ile Asp Val Ile Leu Ala Ala Ile	
130 135 140	
Val Gly Phe Glu Ser Gly Pro Arg Ile Gly Lys Ala Ile Tyr Gly Ser	
145 150 155 160	

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Asp Leu Leu Asn Asn Gly Trp His Cys Gly Ala Val Tyr Gly Ala Pro
 165 170 175
 Ala Gly Ala Leu Ala Thr Gly Lys Leu Phe Gly Leu Thr Pro Asp Ser
 180 185 190
 Met Glu Asp Ala Leu Gly Ile Ala Cys Thr Gln Ala Cys Gly Leu Met
 195 200 205
 Ser Ala Gln Tyr Gly Gly Met Val Lys Arg Val Gln His Gly Phe Ala
 210 215 220
 Ala Arg Asn Gly Leu Leu Gly Gly Leu Leu Ala His Gly Gly Tyr Glu
 225 230 235 240
 Ala Met Lys Gly Val Leu Glu Arg Ser Tyr Gly Gly Phe Leu Lys Met
 245 250 255
 Phe Thr Lys Gly Asn Gly Arg Glu Pro Pro Tyr Lys Glu Glu Glu Val
 260 265 270
 Val Ala Gly Leu Gly Ser Phe Trp His Thr Phe Thr Ile Arg Ile Lys
 275 280 285
 Leu Tyr Ala Cys Cys Gly Leu Val His Gly Pro Val Glu Ala Ile Glu
 290 295 300
 Asn Leu Gln Gly Arg Tyr Pro Glu Leu Leu Asn Arg Ala Asn Leu Ser
 305 310 315 320
 Asn Ile Arg His Val His Val Gln Leu Ser Thr Ala Ser Asn Ser His
 325 330 335
 Cys Gly Trp Ile Pro Glu Glu Arg Pro Ile Ser Ser Ile Ala Gly Gln
 340 345 350
 Met Ser Val Ala Tyr Ile Leu Ala Val Gln Leu Val Asp Gln Gln Cys
 355 360 365
 Leu Leu Ser Gln Phe Ser Glu Phe Asp Asp Asn Leu Glu Arg Pro Glu
 370 375 380
 Val Trp Asp Leu Ala Arg Lys Val Thr Ser Ser Gln Ser Glu Glu Phe
 385 390 395 400
 Asp Gln Asp Gly Asn Cys Leu Ser Ala Gly Arg Val Arg Ile Glu Phe
 405 410 415
 Asn Asp Gly Ser Ser Ile Thr Glu Ser Val Glu Lys Pro Leu Gly Val
 420 425 430
 Lys Glu Pro Met Pro Asn Glu Arg Ile Leu His Lys Tyr Arg Thr Leu
 435 440 445
 Ala Gly Ser Val Thr Asp Glu Ser Arg Val Lys Glu Ile Glu Asp Leu
 450 455 460
 Val Leu Gly Leu Asp Arg Leu Thr Asp Ile Ser Pro Leu Leu Glu Leu
 465 470 475 480
 Leu Asn Cys Pro Val Lys Ser Pro Leu Val
 485 490

<210> SEQ ID NO 13
 <211> LENGTH: 861
 <212> TYPE: DNA
 <213> ORGANISM: Aspergillus terreus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(858)

<400> SEQUENCE: 13

atg	agt	att	caa	cat	ttc	cgt	gtc	gcc	ctt	att	ccc	ttt	ttt	gcg	gca	48
Met	Ser	Ile	Gln	His	Phe	Arg	Val	Ala	Leu	Ile	Pro	Phe	Phe	Ala	Ala	
1				5					10					15		
ttt	tgc	ctt	cct	gtt	ttt	gct	cac	cca	gaa	acg	ctg	gtg	aaa	gta	aaa	96

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Phe	Cys	Leu	Pro	Val	Phe	Ala	His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	
			20					25					30			
gat	gct	gaa	gat	cag	ttg	ggg	gca	cga	gtg	ggg	tac	atc	gaa	ctg	gat	144
Asp	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	
		35					40					45				
ctc	aac	agc	ggg	aag	atc	ctt	gag	agt	ttt	cgc	ccc	gaa	gaa	cgt	ttt	192
Leu	Asn	Ser	Gly	Lys	Ile	Leu	Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	
	50					55					60					
cca	atg	atg	agc	act	ttt	aaa	ggt	ctg	cta	tgt	ggc	gcg	gta	tta	tcc	240
Pro	Met	Met	Ser	Thr	Phe	Lys	Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	
	65				70					75				80		
cgt	att	gac	gcc	ggg	caa	gag	caa	ctc	ggg	cgc	cgc	ata	cac	tat	tct	288
Arg	Ile	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	
			85					90						95		
cag	aat	gac	ttg	ggt	gag	tac	tca	cca	gtc	aca	gaa	aag	cat	ctt	acg	336
Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	
			100					105						110		
gat	ggc	atg	aca	gta	aga	gaa	tta	tgc	agt	gct	gcc	ata	acc	atg	agt	384
Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	
			115				120					125				
gat	aac	act	gcg	gcc	aac	tta	ctt	ctg	aca	acg	atc	gga	gga	ccg	aag	432
Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	Lys	
	130				135						140					
gag	cta	acc	gct	ttt	ttg	cac	aac	atg	ggg	gat	cat	gta	act	cgc	ctt	480
Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	Arg	Leu	
	145				150					155					160	
gat	cgt	tgg	gaa	ccg	gag	ctg	aat	gaa	gcc	ata	cca	aac	gac	gag	cgt	528
Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	
			165					170						175		
gac	acc	acg	atg	cct	gta	gca	atg	gca	aca	acg	ttg	cgc	aaa	cta	tta	576
Asp	Thr	Thr	Met	Pro	Val	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	
			180					185						190		
act	ggc	gaa	cta	ctt	act	cta	gct	tcc	cgg	caa	caa	tta	ata	gac	tgg	624
Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	
	195					200						205				
atg	gag	gcg	gat	aaa	gtt	gca	gga	cca	ctt	ctg	cgc	tgc	gcc	ctt	ccg	672
Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	
	210					215					220					
gct	ggc	tgg	ttt	att	gct	gat	aaa	tct	gga	gcc	ggg	gag	cgt	ggg	tct	720
Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	
	225				230					235				240		
cgc	ggg	atc	att	gca	gca	ctg	ggg	cca	gat	ggg	aag	ccc	tcc	cgt	atc	768
Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	
				245				250						255		
gta	gtt	atc	tac	acg	acg	ggg	agt	cag	gca	act	atg	gat	gaa	cga	aat	816
Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	
			260					265					270			
aga	cag	atc	gct	gag	ata	ggg	gcc	tca	ctg	att	aag	cat	tgg	taa		861
Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp			
			275				280						285			

<210> SEQ ID NO 14

<211> LENGTH: 286

<212> TYPE: PRT

<213> ORGANISM: Aspergillus terreus

<400> SEQUENCE: 14

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys

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tein consists of the amino acid sequence of a protein capable of transporting di/tricarboxylic acids from the mitochondrion, wherein the nucleotide sequence encodes a protein of the amino acid sequence SEQ ID NO:14.

10. The host cells of claim **1**, wherein the nucleic acid 5 encoding itaconate transporter comprises SEQ ID NO:2 or a nucleotide sequence at least 95% identical thereto or SEQ ID NO:5.

11. The host cells of claim **10**, wherein the nucleic acid encoding itaconate transporter comprises SEQ ID NO:2 or 10 SEQ ID NO:5.

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